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(57) Abstract			
<p>The present invention provides human proteins having hydrophobic domains, DNAs coding for these proteins, and expression vectors for these DNAs as well as eucaryotic cells expressing these DNAs.</p>			

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DESCRIPTION

Human Proteins Having Hydrophobic
Domains and DNAs Encoding These Proteins

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TECHNICAL FIELD

The present invention relates to human proteins having hydrophobic domains, DNAs coding for these proteins, and expression vectors for these DNAs as well as eucaryotic cells expressing these DNAs. The proteins of the present invention can be employed as pharmaceuticals or as antigens for preparing antibodies against these proteins. The human cDNAs of the present invention can be utilized as probes for the genetic diagnosis and gene sources for the gene therapy. Furthermore, the cDNAs can be utilized as gene sources for large-scale production of the proteins encoded by these cDNAs. Cells into which these genes are introduced to express secretory proteins and membrane proteins in large amounts can be utilized for detection of the corresponding receptors and ligands, screening of novel low-molecular pharmaceuticals, and so on.

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BACKGROUND ART

Cells secrete many proteins outside the cells. These secretory proteins play important roles for the proliferation control, the differentiation induction, the material transportation, the biological protection, etc. in the cells. Different from intracellular proteins, the secretory proteins exert their actions outside the cells, whereby they can be administered in the intracorporeal manner such as the injection or the drip, so that there are

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hidden potentialities as medicines. In fact, a number of human secretory proteins such as interferons, interleukins, erythropoietin, thrombolytic agents, etc. have been currently employed as medicines. In addition, secretory proteins other than those described above have been undergoing clinical trials to develop as pharmaceuticals. Because it has been conceived that the human cells still produce many unknown secretory proteins, availability of these secretory proteins as well as genes coding for them is expected to lead to development of novel pharmaceuticals utilizing these proteins.

On the other hand, membrane proteins play important roles, as signal receptors, ion channels, transporters, etc. in the material transportation and the information transmission through the cell membrane. Examples thereof include receptors for a variety of cytokines, ion channels for the sodium ion, the potassium ion, the chloride ion, etc., transporters for saccharides and amino acids, and so on, where the genes for many of them have been cloned already. It has been clarified that abnormalities of these membrane proteins are associated with a number of hitherto-cryptogenic diseases. Therefore, discovery of a new membrane protein is anticipated to lead to elucidation of the causes of many diseases, so that isolation of a new gene coding for the membrane protein has been desired.

Heretofore, owing to difficulty in the purification from human cells, these secretory proteins and membrane proteins have been isolated by an approach from the gene side. A general method is the so-called expression cloning which comprises introduction of a cDNA library into eucaryotic cells to express cDNAs and then screening of the cells secreting, or expressing on the surface of membrane,

the objective active protein. However, this method is applicable only to cloning of a gene for a protein with a known function.

5 In general, secretory proteins and membrane proteins possess at least one hydrophobic domain inside the proteins, wherein, after synthesis thereof in the ribosome, this domain works as a secretory signal or remains in the phospholipid membrane to be trapped in the membrane. Accordingly, the evidence of this cDNA for encoding a
10 secretory protein and a membrane protein is provided by determination of the whole base sequence of a full-length cDNA followed by detection of highly hydrophobic domain(s) in the amino acid sequence of the protein encoded by this cDNA.

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OBJECTS OF THE INVENTION

The main object of the present invention is to provide novel human proteins having hydrophobic domains, DNAs coding for these proteins, and expression vectors for these DNAs as
20 well as transformed eucaryotic cells that are capable of expressing these DNAs. This object as well as other objects and advantages of the present invention will become apparent to those skilled in the art from the following description with reference to the accompanying drawings.

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BRIEF DESCRIPTION OF DRAWINGS

Fig. 1 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP01550.

30 Fig. 2 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP02593.

Fig. 3 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10195.

Fig. 4 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10423.

Fig. 5 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10506.

5 Fig. 6 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10507.

Fig. 7 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10548.

10 Fig. 8 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10566.

Fig. 9 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10567.

Fig. 10 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10568.

15 Fig. 11 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP01426.

Fig. 12 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP02515.

20 Fig. 13 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP02575.

Fig. 14 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10357.

Fig. 15 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10447.

25 Fig. 16 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10477.

Fig. 17 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10513.

30 Fig. 18 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10540.

Fig. 19 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10557.

Fig. 20 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10563.

Fig. 21 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP01467.

5 Fig. 22 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP01956.

Fig. 23 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP02545.

10 Fig. 24 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP02551.

Fig. 25 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP02631.

Fig. 26 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP02632.

15 Fig. 27 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10488.

Fig. 28 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10538.

20 Fig. 29 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10542.

Fig. 30 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10571.

Fig. 31 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP01470.

25 Fig. 32 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP02419.

Fig. 33 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP02631.

30 Fig. 34 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP02695.

Fig. 35 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10031.

Fig. 36 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10530.

Fig. 37 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10541.

5 Fig. 38 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10550.

Fig. 39 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10590.

10 Fig. 40 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10591.

Fig. 41 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP01462.

Fig. 42 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP02485.

15 Fig. 43 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP02798.

Fig. 44 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10041.

20 Fig. 45 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10246.

Fig. 46 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10392.

Fig. 47 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10489.

25 Fig. 48 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10519.

Fig. 49 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10531.

30 Fig. 50 illustrates the hydrophobicity/hydrophilicity profile of the protein encoded by clone HP10574.

SUMMARY OF THE INVENTION

As the result of intensive studies, the present inventors have been successful in cloning of cDNAs coding for proteins having hydrophobic domains from the human full-length cDNA bank, thereby completing the present invention.

5 In other words, the present invention provides human proteins having hydrophobic domains, namely proteins comprising any of the amino acid sequences represented by SEQ ID Nos. 1 to 10, 31 to 40, 61 to 70, 91 to 100, and 121 to 130. Moreover, the present invention provides DNAs coding

10 for the above-mentioned proteins, exemplified by cDNAs comprising any of the base sequences represented by SEQ ID Nos. 11 to 20, 41 to 50, 71 to 80, 101 to 110, and 131 to 140, as well as expression vectors that are capable of expressing any of these DNAs by in vitro translation or in

15 eucaryotic cells and transformed eucaryotic cells that are capable of expressing these DNAs and of producing the above-mentioned proteins.

DETAILED DESCRIPTION OF THE INVENTION

20 The proteins of the present invention can be obtained, for example, by a method for isolation from human organs, cell lines, etc., a method for preparation of peptides by the chemical synthesis, or a method for production with the recombinant DNA technology using the DNAs coding for the

25 hydrophobic domains of the present invention, among which the method for production with the recombinant DNA technology is employed preferably. For instance, in vitro expression of the proteins can be achieved by preparation of an RNA by in vitro transcription from a vector having one of

30 the cDNAs of the present invention, followed by in vitro translation using this RNA as a template. Also, introduction of the translated region into a suitable expression vector

by the method known in the art leads to expression of a large amount of the encoded protein in prokaryotic cells such as *Escherichia coli*, *Bacillus subtilis*, etc., and eucaryotic cells such as yeasts, insect cells, mammalian cells, etc.

In the case where one of the proteins of the present invention is produced by expressing the DNA by in vitro translation, the protein of the present invention can be produced in vitro, when the translated region of this cDNA is introduced into a vector having an RNA polymerase promoter, followed by addition of the vector to an in vitro translation system such as a rabbit reticulocyte lysate or a wheat germ extract, containing an RNA polymerase corresponding to the promoter. RNA polymerase promoters are exemplified by T7, T3, SP6, and the like. The vectors containing these RNA polymerase promoters are exemplified by pKA1, pCDM8, pT3/T7 18, pT7/3 19, pBluescript II, and so on. Furthermore, the protein of the present invention can be expressed as the secreted form or the form incorporated into the microsome membrane, when a canine pancreas microsome or the like is added to the reaction system.

In the case where one of the protein of the present invention is produced by expressing the DNA in a microorganism such as *Escherichia coli* etc., a recombinant expression vector bearing the translated region of the cDNA of the present invention is constructed in an expression vector having an origin which can be replicated in the microorganism, a promoter, a ribosome-binding site, a cDNA-cloning site, a terminator etc. and, after transformation of the host cells with this expression vector, the resulting transformant is incubated, whereby the protein encoded by said cDNA can be produced on a large scale in the

microorganism. In this case, a protein fragment containing any region can be obtained by carrying out the expression with inserting an initiation codon and a termination codon in front of and behind the selected translated region.

5 Alternatively, a fusion protein with another protein can be expressed. Only the portion of the protein encoded by this cDNA can be obtained by cleavage of this fusion protein with a suitable protease. The expression vector for *Escherichia coli* is exemplified by the pUC series, pBluescript II, the
10 pET expression system, the pGEX expression system, and so on.

In the case where one of the proteins of the present invention is produced by expressing the DNA in eucaryotic cells, the protein of the present invention can be produced as a secretory protein or as a membrane protein on the cell-
15 membrane surface, when the translated region of this cDNA is introduced into an expression vector for eucaryotic cells that has a promoter, a splicing region, a poly(A) addition site, etc., followed by introduction into the eucaryotic cells. The expression vector is exemplified by pKA1,
20 pED6dpc2, pCDM8, pSVK3, pMSG, pSVL, pBK-CMV, pBK-RSV, EBV vector, pRS, pYES2, and so on. Examples of eucaryotic cells to be used in general include mammalian cultured cells such as simian kidney cells COS7, Chinese hamster ovary cells CHO, etc., budding yeasts, fission yeasts, silkworm cells,
25 *Xenopus* oocytes, and so on, but any eucaryotic cells may be used, provided that they are capable of expressing the proteins of the present invention. The expression vector can be introduced into the eucaryotic cells by methods known in the art such as the electroporation method, the calcium
30 phosphate method, the liposome method, the DEAE-dextran method, and so on.

After one of the proteins of the present invention is

expressed in prokaryotic cells or eucaryotic cells, the objective protein can be isolated from the culture and purified by a combination of separation procedures known in the art. Such examples include treatment with a denaturing agent such as urea or a detergent, sonication, enzymatic digestion, salting-out or solvent precipitation, dialysis, centrifugation, ultrafiltration, gel filtration, SDS-PAGE, isoelectric focusing, ion-exchange chromatography, hydrophobic chromatography, affinity chromatography, reverse phase chromatography, and so on.

The proteins of the present invention include peptide fragments (5 amino acid residues or more) containing any partial amino acid sequence in the amino acid sequences represented by SEQ ID Nos. 1. to 10, 31 to 40, 61 to 70, 91 to 100, and 121 to 130. These peptide fragments can be utilized as antigens for preparation of antibodies. Hereupon, among the proteins of the present invention, those having the signal sequences are secreted in the form of mature proteins, after the signal sequences are removed. Therefore, these mature proteins shall come within the scope of the present invention. The N-terminal amino acid sequences of the mature proteins can be easily determined by using the method for the determination of cleavage site of a signal sequence [JP 8-187100 A]. Furthermore, some membrane proteins undergo the processing on the cell surface to be converted to the secretory forms. Such proteins or peptides in the secretory forms shall come within the scope of the present invention. In the case where sugar chain-binding sites are present in the amino acid sequences, expression in appropriate eucaryotic cells affords proteins to which sugar chains are attached. Accordingly, such proteins or peptides to which sugar chains are attached shall come within the

scope of the present invention.

The DNAs of the present invention include all the DNAs coding for the above-mentioned proteins. These DNAs can be obtained by using a method by chemical synthesis, a method
5 by cDNA cloning, and so on.

The cDNAs of the present invention can be cloned, for example, from cDNA libraries derived from the human cells. These cDNAs are synthesized by using as templates poly(A)⁺ RNAs extracted from human cells. The human cells may be
10 cells delivered from the human body, for example, by the operation or may be the cultured cells. The cDNAs can be synthesized by using any method selected from the Okayama-Berg method [Okayama, H. and Berg, P., Mol. Cell. Biol. 2: 161-170 (1982)], the Gubler-Hoffman method [Gubler, U. and
15 Hoffman, J. Gene 25: 263-269 (1983)], and so on, but it is preferred to use the capping method [Kato, S. et al., Gene 150: 243-250 (1994)], as exemplified in Examples, in order to obtain a full-length clone in an effective manner. In addition, commercially available, human cDNA libraries can
20 be utilized. Cloning of the cDNAs of the present invention from the cDNA libraries can be carried out by synthesis of an oligonucleotide on the basis of base sequences of any portion in the cDNA of the present invention, followed by screening using this oligonucleotide as the probe according
25 to the colony or plaque hybridization by a method known in the art. In addition, the cDNA fragments of the present invention can be prepared by synthesis of oligonucleotides which hybridize with both termini of the objective cDNA fragment, followed by the usage of these oligonucleotides as
30 the primers for the RT-PCR method using an mRNA isolated from human cells.

The cDNAs of the present invention are characterized by

comprising either of the base sequences represented by SEQ ID Nos. 11 to 20, 41 to 50, 71 to 80, 101 to 110, and 131 to 140 or the base sequences represented by SEQ ID Nos. 21 to 30, 51 to 60, 81 to 90, 111 to 120, and 141 to 150. Table 1
5 summarizes the clone number (HP number), the cells from which the cDNA was obtained, the total base number of the cDNA, and the number of the amino acid residues of the encoded protein, for each of the cDNAs.

Table 1

SEQ ID No.	HP number	Cells	Base number	Number of amino acid residues
1, 11, 21	HP01550	Stomach cancer	510	125
2, 12, 22	HP02593	Saos-2	697	131
3, 13, 23	HP10195	HT-1080	1619	242
4, 14, 24	HP10423	U-2 OS	1066	264
5, 15, 25	HP10506	Stomach cancer	618	112
6, 16, 26	HP10507	Stomach cancer	1021	146
7, 17, 27	HP10548	Stomach cancer	1432	344
8, 18, 28	HP10566	Stomach cancer	601	97
9, 19, 29	HP10567	Stomach cancer	585	124
10, 20, 30	HP10568	Stomach cancer	1100	327
31, 41, 51	HP01426	Stomach cancer	1065	313
32, 42, 52	HP02515	Saos-2	937	229
33, 43, 53	HP02575	Saos-2	1678	467
34, 44, 54	HP10357	Stomach cancer	467	99
35, 45, 55	HP10447	Liver	875	189
36, 46, 56	HP10477	Liver	1256	363
37, 47, 57	HP10513	Stomach cancer	884	249
38, 48, 58	HP10540	Saos-2	589	98
39, 49, 59	HP10557	Stomach cancer	673	172
40, 50, 60	HP10563	Saos-2	1425	120
61, 71, 81	HP01467	HT-1080	1436	307
62, 72, 82	HP01956	Liver	997	183
63, 73, 83	HP02545	Saos-2	1753	327
64, 74, 84	HP02551	Saos-2	1117	223
65, 75, 85	HP02631	Saos-2	1380	48
66, 76, 86	HP02632	HT-1080	1503	371
67, 77, 87	HP10488	Liver	733	90
68, 78, 88	HP10538	Saos-2	3768	499
69, 79, 89	HP10542	Stomach cancer	770	106
70, 80, 90	HP10571	Stomach cancer	1229	152

91, 101, 111	HP01470	Stomach cancer	1619	358
92, 102, 112	HP02419	Stomach cancer	2054	226
93, 103, 113	HP02631	Saos-2	1380	195
94, 104, 114	HP02695	Stomach cancer	1292	339
95, 105, 115	HP10031	Saos-2	2168	487
96, 106, 116	HP10530	Saos-2	1357	393
97, 107, 117	HP10541	Stomach cancer	711	196
98, 108, 118	HP10550	Stomach cancer	651	107
99, 109, 119	HP10590	HT-1080	1310	350
100, 110, 120	HP10591	HT-1080	1400	107
121, 131, 141	HP01462	HT-1080	2050	483
122, 132, 142	HP02485	Stomach cancer	2746	334
123, 133, 143	HP02798	HT-1080	1136	267
124, 134, 144	HP10041	Saos-2	619	106
125, 135, 145	HP10246	KB	864	224
126, 136, 146	HP10392	U-2 OS	1527	258
127, 137, 147	HP10489	Stomach cancer	659	110
128, 138, 148	HP10519	Stomach cancer	710	91
129, 139, 149	HP10531	Saos-2	2182	344
130, 140, 150	HP10574	Stomach cancer	2773	428

Hereupon, the same clones as the cDNAs of the present invention can be easily obtained by screening of the cDNA libraries constructed from the human cell lines or human tissues utilized in the present invention by the use of an oligonucleotide probe synthesized on the basis of the cDNA base sequence described in any of SEQ ID Nos. 11 to 30, 41 to 60, 71 to 90, 101 to 120, and 131 to 150.

In general, the polymorphism due to the individual difference is frequently observed in human genes. Accordingly, any cDNA in which one or plural nucleotides are inserted, deleted and/or substituted with other nucleotides in SEQ ID Nos. 11 to 30, 41 to 60, 71 to 90, 101 to 120, and

131 to 150 shall come within the scope of the present invention.

5 In a similar manner, any protein in which one or plural amino acids are inserted, deleted and/or substituted with other amino acids shall come within the scope of the present invention, as far as the protein possesses the activity of any protein having the amino acid sequences represented by SEQ ID Nos. 1 to 10, 31 to 40, 61 to 70, 91 to 100, and 121 to 130.

10 The cDNAs of the present invention include cDNA fragments (10 bp or more) containing any partial base sequence in the base sequences represented by SEQ ID Nos. 11 to 20, 41 to 50, 71 to 80, 101 to 110, and 131 to 140 or in the base sequences represented by SEQ ID Nos. 21 to 30, 51 to 60, 81 to 90, 111 to 120, and 141 to 150. Also, DNA
15 fragments consisting of a sense strand and an anti-sense strand shall come within this scope. These DNA fragments can be utilized as the probes for the genetic diagnosis.

20 In addition to the activities and uses described above, the polynucleotides and proteins of the present invention may exhibit one or more of the uses or biological activities (including those associated with assays cited herein) identified below. Uses or activities described for proteins of the present invention may be provided by administration
25 or use of such proteins or by administration or use of polynucleotides encoding such proteins (such as, for example, in gene therapies or vectors suitable for introduction of DNA).

Research Uses and Utilities

30 The polynucleotides provided by the present invention can be used by the research community for various purposes. The polynucleotides can be used to express recombinant

protein for analysis, characterization or therapeutic use; as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in disease states); as molecular weight markers on Southern gels; as chromosome markers or tags (when labeled) to identify chromosomes or to map related gene positions; to compare with endogenous DNA sequences in patients to identify potential genetic disorders; as probes to hybridize and thus discover novel, related DNA sequences; as a source of information to derive PCR primers for genetic fingerprinting; as a probe to "subtract-out" known sequences in the process of discovering other novel polynucleotides; for selecting and making oligomers for attachment to a "gene chip" or other support, including for examination of expression patterns; to raise anti-protein antibodies using DNA immunization techniques; and as an antigen to raise anti-DNA antibodies or elicit another immune response. Where the polynucleotide encodes a protein which binds or potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the polynucleotide can also be used in interaction trap assays (such as, for example, that described in Gyuris et al., Cell 75:791-803 (1993)) to identify polynucleotides encoding the other protein with which binding occurs or to identify inhibitors of the binding interaction.

The proteins provided by the present invention can similarly be used in assay to determine biological activity, including in a panel of multiple proteins for high-throughput screening; to raise antibodies or to elicit another immune response; as a reagent (including the labeled reagent) in assays designed to quantitatively determine

levels of the protein (or its receptor) in biological fluids; as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in a disease state); and, of course, to isolate correlative receptors or ligands. Where the protein binds or potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the protein can be used to identify the other protein with which binding occurs or to identify inhibitors of the binding interaction. Proteins involved in these binding interactions can also be used to screen for peptide or small molecule inhibitors or agonists of the binding interaction.

Any or all of these research utilities are capable of being developed into reagent grade or kit format for commercialization as research products.

Methods for performing the uses listed above are well known to those skilled in the art. References disclosing such methods include without limitation "Molecular Cloning: A Laboratory Manual", 2d ed., Cold Spring Harbor Laboratory Press, Sambrook, J., E.F. Fritsch and T. Maniatis eds., 1989, and "Methods in Enzymology: Guide to Molecular Cloning Techniques", Academic Press, Berger, S.L. and A.R. Kimmel eds., 1987.

Nutritional Uses

Polynucleotides and proteins of the present invention can also be used as nutritional sources or supplements. Such uses include without limitation use as a protein or amino acid supplement, use as a carbon source, use as a nitrogen source and use as a source of carbohydrate. In such cases the protein or polynucleotide of the invention can be added to the feed of a particular organism or can be

administered as a separate solid or liquid preparation, such as in the form of powder, pills, solutions, suspensions or capsules. In the case of microorganisms, the protein or polynucleotide of the invention can be added to the medium
5 in or on which the microorganism is cultured.

Cytokine and Cell Proliferation/Differentiation
Activity

A protein of the present invention may exhibit cytokine, cell proliferation (either inducing or inhibiting) or cell
10 differentiation (either inducing or inhibiting) activity or may induce production of other cytokines in certain cell populations. Many protein factors discovered to date, including all known cytokines, have exhibited activity in one or more factor dependent cell proliferation assays, and
15 hence the assays serve as a convenient confirmation of cytokine activity. The activity of a protein of the present invention is evidenced by any one of a number of routine factor dependent cell proliferation assays for cell lines including, without limitation, 32D, DA2, DA1G, T10, B9,
20 B9/11, BaF3, MC9/G, M+ (preB M+), 2E8, RB5, DA1, 123, T1165, HT2, CTLL2, TF-1, Mo7e and CMK.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for T-cell or thymocyte proliferation include
25 without limitation those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7,
30 Immunologic studies in Humans); Takai et al., J. Immunol. 137:3494-3500, 1986; Bertagnolli et al., J. Immunol. 145:1706-1712, 1990; Bertagnolli et al., Cellular

Immunology 133:327-341, 1991; Bertagnolli, et al., J. Immunol. 149:3778-3783, 1992; Bowman et al., J. Immunol. 152: 1756-1761, 1994.

5 Assays for cytokine production and/or proliferation of spleen cells, lymph node cells or thymocytes include, without limitation, those described in: Polyclonal T cell stimulation, Kruisbeek, A.M. and Shevach, E.M. In Current Protocols in Immunology. J.E.e.a. Coligan eds. Vol 1 pp. 3.12.1-3.12.14, John Wiley and Sons, Toronto. 1994; and
10 Measurement of mouse and human Interferon γ , Schreiber, R.D. In Current Protocols in Immunology. J.E.e.a. Coligan eds. Vol 1 pp. 6.8.1-6.8.8, John Wiley and Sons, Toronto. 1994.

Assays for proliferation and differentiation of hematopoietic and lymphopoietic cells include, without
15 limitation, those described in: Measurement of Human and Murine Interleukin 2 and Interleukin 4, Bottomly, K., Davis, L.S. and Lipsky, P.E. In Current Protocols in Immunology. J.E.e.a. Coligan eds. Vol 1 pp. 6.3.1-6.3.12, John Wiley and Sons, Toronto. 1991; deVries et al., J. Exp. Med. 173:1205-
20 1211, 1991; Moreau et al., Nature 336:690-692, 1988; Greenberger et al., Proc. Natl. Acad. Sci. U.S.A. 80:2931-2938, 1983; Measurement of mouse and human interleukin 6-
Nordan, R. In Current Protocols in Immunology. J.E.e.a. Coligan eds. Vol 1 pp. 6.6.1-6.6.5, John Wiley and Sons,
25 Toronto. 1991; Smith et al., Proc. Natl. Acad. Sci. U.S.A. 83:1857-1861, 1986; Measurement of human Interleukin 11 -
Bennett, F., Giannotti, J., Clark, S.C. and Turner, K. J. In Current Protocols in Immunology. J.E.e.a. Coligan eds. Vol 1 pp. 6.15.1 John Wiley and Sons, Toronto. 1991;
30 Measurement of mouse and human Interleukin 9 - Ciarletta, A., Giannotti, J., Clark, S.C. and Turner, K.J. In Current Protocols in Immunology. J.E.e.a. Coligan eds. Vol 1 pp.

6.13.1, John Wiley and Sons, Toronto. 1991.

Assays for T-cell clone responses to antigens (which will identify, among others, proteins that affect APC-T cell interactions as well as direct T-cell effects by measuring proliferation and cytokine production) include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function; Chapter 6, Cytokines and their cellular receptors; Chapter 7, Immunologic studies in Humans); Weinberger et al., Proc. Natl. Acad. Sci. USA 77:6091-6095, 1980; Weinberger et al., Eur. J. Immun. 11:405-411, 1981; Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988.

Immune Stimulating or Suppressing Activity

A protein of the present invention may also exhibit immune stimulating or immune suppressing activity, including without limitation the activities for which assays are described herein. A protein may be useful in the treatment of various immune deficiencies and disorders (including severe combined immunodeficiency (SCID)), e.g., in regulating (up or down) growth and proliferation of T and/or B lymphocytes, as well as effecting the cytolytic activity of NK cells and other cell populations. These immune deficiencies may be genetic or be caused by viral (e.g., HIV) as well as bacterial or fungal infections, or may result from autoimmune disorders. More specifically, infectious diseases caused by viral, bacterial, fungal or other infection may be treatable using a protein of the present invention, including infections by HIV, hepatitis viruses, herpesviruses, mycobacteria, Leishmania spp., malaria spp.

and various fungal infections such as candidiasis. Of course, in this regard, a protein of the present invention may also be useful where a boost to the immune system generally may be desirable, i.e., in the treatment of cancer.

5 Autoimmune disorders which may be treated using a protein of the present invention include, for example, connective tissue disease, multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation, Guillain-Barre syndrome, autoimmune
10 thyroiditis, insulin dependent diabetes mellitus, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. Such a protein of the present invention may also to be useful in the treatment of allergic reactions and conditions, such as asthma (particularly
15 allergic asthma) or other respiratory problems. Other conditions, in which immune suppression is desired (including, for example, organ transplantation), may also be treatable using a protein of the present invention.

 Using the proteins of the invention it may also be
20 possible to immune responses, in a number of ways. Down regulation may be in the form of inhibiting or blocking an immune response already in progress or may involve preventing the induction of an immune response. The functions of activated T cells may be inhibited by
25 suppressing T cell responses or by inducing specific tolerance in T cells, or both. Immunosuppression of T cell responses is generally an active, non-antigen-specific, process which requires continuous exposure of the T cells to the suppressive agent. Tolerance, which involves inducing
30 non-responsiveness or anergy in T cells, is distinguishable from immunosuppression in that it is generally antigen-specific and persists after exposure to the tolerizing agent

has ceased. Operationally, tolerance can be demonstrated by the lack of a T cell response upon reexposure to specific antigen in the absence of the tolerizing agent.

5 Down regulating or preventing one or more antigen functions (including without limitation B lymphocyte antigen functions (such as , for example, B7)), e.g., preventing high level lymphokine synthesis by activated T cells, will be useful in situations of tissue, skin and organ transplantation and in graft-versus-host disease (GVHD).
10 For example, blockage of T cell function should result in reduced tissue destruction in tissue transplantation. Typically, in tissue transplants, rejection of the transplant is initiated through its recognition as foreign by T cells, followed by an immune reaction that destroys the
15 transplant. The administration of a molecule which inhibits or blocks interaction of a B7 lymphocyte antigen with its natural ligand(s) on immune cells (such as a soluble, monomeric form of a peptide having B7-2 activity alone or in conjunction with a monomeric form of a peptide having an
20 activity of another B lymphocyte antigen (e.g., B7-1, B7-3) or blocking antibody), prior to transplantation can lead to the binding of the molecule to the natural ligand(s) on the immune cells without transmitting the corresponding costimulatory signal. Blocking B lymphocyte antigen
25 function in this matter prevents cytokine synthesis by immune cells, such as T cells, and thus acts as an immunosuppressant. Moreover, the lack of costimulation may also be sufficient to anergize the T cells, thereby inducing tolerance in a subject. Induction of long-term tolerance by
30 B lymphocyte antigen-blocking reagents may avoid the necessity of repeated administration of these blocking reagents. To achieve sufficient immunosuppression or

tolerance in a subject, it may also be necessary to block the function of a combination of B lymphocyte antigens.

5 The efficacy of particular blocking reagents in preventing organ transplant rejection or GVHD can be assessed using animal models that are predictive of efficacy in humans. Examples of appropriate systems which can be used include allogeneic cardiac grafts in rats and xenogeneic pancreatic islet cell grafts in mice, both of which have been used to examine the immunosuppressive effects of CTLA4Ig fusion proteins in vivo as described in 10 Lenschow et al., Science 257:789-792 (1992) and Turka et al., Proc. Natl. Acad. Sci USA, 89:11102-11105 (1992). In addition, murine models of GVHD (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 846-847) can be used to determine the effect of blocking B lymphocyte 15 antigen function in vivo on the development of that disease.

Blocking antigen function may also be therapeutically useful for treating autoimmune diseases. Many autoimmune disorders are the result of inappropriate activation of T 20 cells that are reactive against self tissue and which promote the production of cytokines and autoantibodies involved in the pathology of the diseases. Preventing the activation of autoreactive T cells may reduce or eliminate disease symptoms. Administration of reagents which block 25 costimulation of T cells by disrupting receptor:ligand interactions of B lymphocyte antigens can be used to inhibit T cell activation and prevent production of autoantibodies or T cell-derived cytokines which may be involved in the disease process. Additionally, blocking reagents may induce 30 antigen-specific tolerance of autoreactive T cells which could lead to long-term relief from the disease. The efficacy of blocking reagents in preventing or alleviating

autoimmune disorders can be determined using a number of well-characterized animal models of human autoimmune diseases. Examples include murine experimental autoimmune encephalitis, systemic lupus erythmatosis in MRL/lpr/lpr mice or NZB hybrid mice, murine autoimmune collagen arthritis, diabetes mellitus in NOD mice and BB rats, and murine experimental myasthenia gravis (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 840-856).

Upregulation of an antigen function (preferably a B lymphocyte antigen function), as a means of up regulating immune responses, may also be useful in therapy. Upregulation of immune responses may be in the form of enhancing an existing immune response or eliciting an initial immune response. For example, enhancing an immune response through stimulating B lymphocyte antigen function may be useful in cases of viral infection. In addition, systemic viral diseases such as influenza, the commoncold, and encephalitis might be alleviated by the administration of stimulatory forms of B lymphocyte antigens systemically.

Alternatively, anti-viral immune responses may be enhanced in an infected patient by removing T cells from the patient, costimulating the T cells in vitro with viral antigen-pulsed APCs either expressing a peptide of the present invention or together with a stimulatory form of a soluble peptide of the present invention and reintroducing the in vitro activated T cells into the patient. Another method of enhancing anti-viral immune responses would be to isolate infected cells from a patient, transfect them with a nucleic acid encoding a protein of the present invention as described herein such that the cells express all or a portion of the protein on their surface, and reintroduce the

transfected cells into the patient. The infected cells would now be capable of delivering a costimulatory signal to, and thereby activate, T cells in vivo.

5 In another application, up regulation or enhancement of antigen function (preferably B lymphocyte antigen function) may be useful in the induction of tumor immunity. Tumor cells (e.g., sarcoma, melanoma, lymphoma, leukemia, neuroblastoma, carcinoma) transfected with a nucleic acid encoding at least one peptide of the present invention can
10 be administered to a subject to overcome tumor-specific tolerance in the subject. If desired, the tumor cell can be transfected to express a combination of peptides. For example, tumor cells obtained from a patient can be transfected ex vivo with an expression vector directing the
15 expression of a peptide having B7-2-like activity alone, or in conjunction with a peptide having B7-1-like activity and/or B7-3-like activity. The transfected tumor cells are returned to the patient to result in expression of the peptides on the surface of the transfected cell.
20 Alternatively, gene therapy techniques can be used to target a tumor cell for transfection in vivo.

The presence of the peptide of the present invention having the activity of a B lymphocyte antigen(s) on the surface of the tumor cell provides the necessary
25 costimulation signal to T cells to induce a T cell mediated immune response against the transfected tumor cells. In addition, tumor cells which lack MHC class I or MHC class II molecules, or which fail to reexpress sufficient amounts of MHC class I or MHC class II molecules, can be transfected
30 with nucleic acid encoding all or a portion of (e.g., a cytoplasmic-domain truncated portion) of an MHC class I α chain protein and β microglobulin protein or an MHC class

II chain protein and an MHC class II chain protein to thereby express MHC class I or MHC class II proteins on the cell surface. Expression of the appropriate class I or class II MHC in conjunction with a peptide having the activity of a B lymphocyte antigen (e.g., B7-1, B7-2, B7-3) induces a T cell mediated immune response against the transfected tumor cell. Optionally, a gene encoding an antisense construct which blocks expression of an MHC class II associated protein, such as the invariant chain, can also be cotransfected with a DNA encoding a peptide having the activity of a B lymphocyte antigen to promote presentation of tumor associated antigens and induce tumor specific immunity. Thus, the induction of a T cell mediated immune response in a human subject may be sufficient to overcome tumor-specific tolerance in the subject.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for thymocyte or splenocyte cytotoxicity include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Herrmann et al., Proc. Natl. Acad. Sci. USA 78:2488-2492, 1981; Herrmann et al., J. Immunol. 128:1968-1974, 1982; Handa et al., J. Immunol. 135:1564-1572, 1985; Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Herrmann et al., Proc. Natl. Acad. Sci. USA 78:2488-2492, 1981; Herrmann et al., J. Immunol. 128:1968-1974, 1982; Handa et al., J. Immunol. 135:1564-1572, 1985; Takai et al., J. Immunol. 137:3494-3500, 1986; Bowman et al., J.

Virology 61:1992-1998; Takai et al., J. Immunol. 140:508-512, 1988; Bertagnolli et al., Cellular Immunology 133:327-341, 1991; Brown et al., J. Immunol. 153:3079-3092, 1994.

5 Assays for T-cell-dependent immunoglobulin responses and isotype switching (which will identify, among others, proteins that modulate T-cell dependent antibody responses and that affect Th1/Th2 profiles) include, without limitation, those described in: Maliszewski, J. Immunol. 144:3028-3033, 1990; and Assays for B cell function: In
10 vitro antibody production, Mond, J.J. and Brunswick, M. In Current Protocols in Immunology. J.E.e.a. Coligan eds. Vol 1 pp. 3.8.1-3.8.16, John Wiley and Sons, Toronto. 1994.

Mixed lymphocyte reaction (MLR) assays (which will identify, among others, proteins that generate predominantly
15 Th1 and CTL responses) include, without limitation, those described in: Current Protocols in Immunology, Ed. by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse
20 Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Bertagnolli et al., J. Immunol. 149:3778-3783, 1992.

Dendritic cell-dependent assays (which will identify,
25 among others, proteins expressed by dendritic cells that activate naive T-cells) include, without limitation, those described in: Guery et al., J. Immunol. 134:536-544, 1995; Inaba et al., Journal of Experimental Medicine 173:549-559, 1991; Macatonia et al., Journal of Immunology 154:5071-5079, 1995; Porgador et al., Journal of Experimental Medicine
30 182:255-260, 1995; Nair et al., Journal of Virology 67:4062-4069, 1993; Huang et al., Science 264:961-965,

1994; Macatonia et al., Journal of Experimental Medicine 169:1255-1264, 1989; Bhardwaj et al., Journal of Clinical Investigation 94:797-807, 1994; and Inaba et al., Journal of Experimental Medicine 172:631-640, 1990.

5 Assays for lymphocyte survival/apoptosis (which will identify, among others, proteins that prevent apoptosis after superantigen induction and proteins that regulate lymphocyte homeostasis) include, without limitation, those described in: Darzynkiewicz et al., Cytometry 13:795-808,
10 1992; Gorczyca et al., Leukemia 7:659-670, 1993; Gorczyca et al., Cancer Research 53:1945-1951, 1993; Itoh et al., Cell 66:233-243, 1991; Zacharchuk, Journal of Immunology 145:4037-4045, 1990; Zamai et al., Cytometry 14:891-897, 1993; Gorczyca et al., International Journal of Oncology
15 1:639-648, 1992.

 Assays for proteins that influence early steps of T-cell commitment and development include, without limitation, those described in: Antica et al., Blood 84:111-117, 1994; Fine et al., Cellular Immunology 155:111-122, 1994; Galy et al., Blood 85:2770-2778, 1995; Toki et al., Proc. Nat. Acad Sci. USA 88:7548-7551, 1991.

Hematopoiesis Regulating Activity

 A protein of the present invention may be useful in regulation of hematopoiesis and, consequently, in the
25 treatment of myeloid or lymphoid cell deficiencies. Even marginal biological activity in support of colony forming cells or of factor-dependent cell lines indicates involvement in regulating hematopoiesis, e.g. in supporting the growth and proliferation of erythroid progenitor cells
30 alone or in combination with other cytokines, thereby indicating utility, for example, in treating various anemias or for use in conjunction with irradiation/chemotherapy to

stimulate the production of erythroid precursors and/or erythroid cells; in supporting the growth and proliferation of myeloid cells such as granulocytes and monocytes/macrophages (i.e., traditional CSF activity) useful, for example, in conjunction with chemotherapy to prevent or treat consequent myelo-suppression; in supporting the growth and proliferation of megakaryocytes and consequently of platelets thereby allowing prevention or treatment of various platelet disorders such as thrombocytopenia, and generally for use in place of or complimentary to platelet transfusions; and/or in supporting the growth and proliferation of hematopoietic stem cells which are capable of maturing to any and all of the above-mentioned hematopoietic cells and therefore find therapeutic utility in various stem cell disorders (such as those usually treated with transplantation, including, without limitation, aplastic anemia and paroxysmal nocturnal hemoglobinuria), as well as in repopulating the stem cell compartment post irradiation/chemotherapy, either in-vivo or ex-vivo (i.e., in conjunction with bone marrow transplantation or with peripheral progenitor cell transplantation (homologous or heterologous)) as normal cells or genetically manipulated for gene therapy.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for proliferation and differentiation of various hematopoietic lines are cited above.

Assays for embryonic stem cell differentiation (which will identify, among others, proteins that influence embryonic differentiation hematopoiesis) include, without limitation, those described in: Johansson et al. Cellular Biology 15:141-151, 1995; Keller et al., Molecular and

Cellular Biology 13:473-486, 1993; McClanahan et al., Blood 81:2903-2915, 1993.

Assays for stem cell survival and differentiation (which will identify, among others, proteins that regulate lympho-hematopoiesis) include, without limitation, those described in: Methylcellulose colony forming assays, Freshney, M.G. In Culture of Hematopoietic Cells. R.I. Freshney, et al. eds. Vol pp. 265-268, Wiley-Liss, Inc., New York, NY. 1994; Hirayama et al., Proc. Natl. Acad. Sci. USA 89:5907-5911, 1992; Primitive hematopoietic colony forming cells with high proliferative potential, McNiece, I.K. and Briddell, R.A. In Culture of Hematopoietic Cells. R.I. Freshney, et al. eds. Vol pp. 23-39, Wiley-Liss, Inc., New York, NY. 1994; Neben et al., Experimental Hematology 22:353-359, 1994; Cobblestone area forming cell assay, Ploemacher, R.E. In Culture of Hematopoietic Cells. R.I. Freshney, et al. eds. Vol pp. 1-21, Wiley-Liss, Inc., New York, NY. 1994; Long term bone marrow cultures in the presence of stromal cells, Spooncer, E., Dexter, M. and Allen, T. In Culture of Hematopoietic Cells. R.I. Freshney, et al. eds. Vol pp. 163-179, Wiley-Liss, Inc., New York, NY. 1994; Long term culture initiating cell assay, Sutherland, H.J. In Culture of Hematopoietic Cells. R.I. Freshney, et al. eds. Vol pp. 139-162, Wiley-Liss, Inc., New York, NY. 1994.

Tissue Growth Activity

A protein of the present invention also may have utility in compositions used for bone, cartilage, tendon, ligament and/or nerve tissue growth or regeneration, as well as for wound healing and tissue repair and replacement, and in the treatment of burns, incisions and ulcers.

A protein of the present invention, which induces cartilage and/or bone growth in circumstances where bone is

not normally formed, has application in the healing of bone fractures and cartilage damage or defects in humans and other animals. Such a preparation employing a protein of the invention may have prophylactic use in closed as well as open fracture reduction and also in the improved fixation of artificial joints. De novo bone formation induced by an osteogenic agent contributes to the repair of congenital, trauma induced, or oncologic resection induced craniofacial defects, and also is useful in cosmetic plastic surgery.

A protein of this invention may also be used in the treatment of periodontal disease, and in other tooth repair processes. Such agents may provide an environment to attract bone-forming cells, stimulate growth of bone-forming cells or induce differentiation of progenitors of bone-forming cells. A protein of the invention may also be useful in the treatment of osteoporosis or osteoarthritis, such as through stimulation of bone and/or cartilage repair or by blocking inflammation or processes of tissue destruction (collagenase activity, osteoclast activity, etc.) mediated by inflammatory processes.

Another category of tissue regeneration activity that may be attributable to the protein of the present invention is tendon/ligament formation. A protein of the present invention, which induces tendon/ligament-like tissue or other tissue formation in circumstances where such tissue is not normally formed, has application in the healing of tendon or ligament tears, deformities and other tendon or ligament defects in humans and other animals. Such a preparation employing a tendon/ligament-like tissue inducing protein may have prophylactic use in preventing damage to tendon or ligament tissue, as well as use in the improved fixation of tendon or ligament to bone or other tissues, and

in repairing defects to tendon or ligament tissue. De novo tendon/ligament-like tissue formation induced by a composition of the present invention contributes to the repair of congenital, trauma induced, or other tendon or ligament defects of other origin, and is also useful in cosmetic plastic surgery for attachment or repair of tendons or ligaments. The compositions of the present invention may provide an environment to attract tendon or ligament-forming cells, stimulate growth of tendon- or ligament-forming cells, induce differentiation of progenitors of tendon- or ligament-forming cells, or induce growth of tendon/ligament cells or progenitors ex vivo for return in vivo to effect tissue repair. The compositions of the invention may also be useful in the treatment of tendinitis, carpal tunnel syndrome and other tendon or ligament defects. The compositions may also include an appropriate matrix and/or sequestering agent as a carrier as is well known in the art.

The protein of the present invention may also be useful for proliferation of neural cells and for regeneration of nerve and brain tissue, i.e. for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders, which involve degeneration, death or trauma to neural cells or nerve tissue. More specifically, a protein may be used in the treatment of diseases of the peripheral nervous system, such as peripheral nerve injuries, peripheral neuropathy and localized neuropathies, and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager syndrome. Further conditions which may be treated in accordance with the present invention include mechanical and traumatic disorders, such as spinal cord disorders, head

trauma and cerebrovascular diseases such as stroke. Peripheral neuropathies resulting from chemotherapy or other medical therapies may also be treatable using a protein of the invention.

5 Proteins of the invention may also be useful to promote better or faster closure of non-healing wounds, including without limitation pressure ulcers, ulcers associated with vascular insufficiency, surgical and traumatic wounds, and the like.

10 It is expected that a protein of the present invention may also exhibit activity for generation or regeneration of other tissues, such as organs (including, for example, pancreas, liver, intestine, kidney, skin, endothelium), muscle (smooth, skeletal or cardiac) and vascular (including
15 vascular endothelium) tissue, or for promoting the growth of cells comprising such tissues. Part of the desired effects may be by inhibition or modulation of fibrotic scarring to allow normal tissue to regenerate. A protein of the invention may also exhibit angiogenic activity.

20 A protein of the present invention may also be useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, and conditions resulting from systemic cytokine damage.

A protein of the present invention may also be useful
25 for promoting or inhibiting differentiation of tissues described above from precursor tissues or cells; or for inhibiting the growth of tissues described above.

The activity of a protein of the invention may, among other means, be measured by the following methods:

30 Assays for tissue generation activity include, without limitation, those described in: International Patent Publication No. WO95/16035 (bone, cartilage, tendon);

International Patent Publication No. WO95/05846 (nerve, neuronal); International Patent Publication No. WO91/07491 (skin, endothelium).

5 Assays for wound healing activity include, without limitation, those described in: Winter, Epidermal Wound Healing, pps. 71-112 (Maibach, HI and Rovee, DT, eds.), Year Book Medical Publishers, Inc., Chicago, as modified by Eaglstein and Mertz, J. Invest. Dermatol 71:382-84 (1978).

Activin/Inhibin Activity

10 A protein of the present invention may also exhibit activin- or inhibin-related activities. Inhibins are characterized by their ability to inhibit the release of follicle stimulating hormone (FSH), while activins and are characterized by their ability to stimulate the release of
15 follicle stimulating hormone (FSH). Thus, a protein of the present invention, alone or in heterodimers with a member of the inhibin family, may be useful as a contraceptive based on the ability of inhibins to decrease fertility in female mammals and decrease spermatogenesis in male mammals.
20 Administration of sufficient amounts of other inhibins can induce infertility in these mammals. Alternatively, the protein of the invention, as a homodimer or as a heterodimer with other protein subunits of the inhibin- group, may be useful as a fertility inducing therapeutic, based upon the
25 ability of activin molecules in stimulating FSH release from cells of the anterior pituitary. See, for example, United States Patent 4,798,885. A protein of the invention may also be useful for advancement of the onset of fertility in sexually immature mammals, so as to increase the lifetime
30 reproductive performance of domestic animals such as cows, sheep and pigs.

The activity of a protein of the invention may, among

other means, be measured by the following methods:

Assays for activin/inhibin activity include, without limitation, those described in: Vale et al., Endocrinology 91:562-572, 1972; Ling et al., Nature 321:779-782, 1986; 5 Vale et al., Nature 321:776-779, 1986; Mason et al., Nature 318:659-663, 1985; Forage et al., Proc. Natl. Acad. Sci. USA 83:3091-3095, 1986.

Chemotactic/Chemokinetic Activity

10 A protein of the present invention may have chemotactic or chemokinetic activity (e.g., act as a chemokine) for mammalian cells, including, for example, monocytes, fibroblasts, neutrophils, T-cells, mast cells, eosinophils, epithelial and/or endothelial cells. Chemotactic and chemokinetic proteins can be used to mobilize or attract a 15 desired cell population to a desired site of action. Chemotactic or chemokinetic proteins provide particular advantages in treatment of wounds and other trauma to tissues, as well as in treatment of localized infections. For example, attraction of lymphocytes, monocytes or 20 neutrophils to tumors or sites of infection may result in improved immune responses against the tumor or infecting agent.

A protein or peptide has chemotactic activity for a particular cell population if it can stimulate, directly or 25 indirectly, the directed orientation or movement of such cell population. Preferably, the protein or peptide has the ability to directly stimulate directed movement of cells. Whether a particular protein has chemotactic activity for a population of cells can be readily determined by employing 30 such protein or peptide in any known assay for cell chemotaxis.

The activity of a protein of the invention may, among

other means, be measured by the following methods:

Assays for chemotactic activity (which will identify proteins that induce or prevent chemotaxis) consist of assays that measure the ability of a protein to induce the migration of cells across a membrane as well as the ability of a protein to induce the adhesion of one cell population to another cell population. Suitable assays for movement and adhesion include, without limitation, those described in: Current Protocols in Immunology, Ed by J.E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 6.12, Measurement of alpha and beta Chemokines 6.12.1-6.12.28; Taub et al. J. Clin. Invest. 95:1370-1376, 1995; Lind et al. APMIS 103:140-146, 1995; Muller et al Eur. J. Immunol. 25: 1744-1748; Gruber et al. J. of Immunol. 152:5860-5867, 1994; Johnston et al. J. of Immunol. 153: 1762-1768, 1994.

Hemostatic and Thrombolytic Activity

A protein of the invention may also exhibit hemostatic or thrombolytic activity. As a result, such a protein is expected to be useful in treatment of various coagulation disorders (including hereditary disorders, such as hemophilias) or to enhance coagulation and other hemostatic events in treating wounds resulting from trauma, surgery or other causes. A protein of the invention may also be useful for dissolving or inhibiting formation of thromboses and for treatment and prevention of conditions resulting therefrom (such as, for example, infarction of cardiac and central nervous system vessels (e.g., stroke).

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assay for hemostatic and thrombolytic activity include,

without limitation, those described in: Linet et al., J. Clin. Pharmacol. 26:131-140, 1986; Burdick et al., Thrombosis Res. 45:413-419, 1987; Humphrey et al., Fibrinolysis 5:71-79 (1991); Schaub, Prostaglandins 35:467-474, 1988.

Receptor/Ligand Activity

A protein of the present invention may also demonstrate activity as receptors, receptor ligands or inhibitors or agonists of receptor/ligand interactions. Examples of such receptors and ligands include, without limitation, cytokine receptors and their ligands, receptor kinases and their ligands, receptor phosphatases and their ligands, receptors involved in cell-cell interactions and their ligands (including without limitation, cellular adhesion molecules (such as selectins, integrins and their ligands) and receptor/ligand pairs involved in antigen presentation, antigen recognition and development of cellular and humoral immune responses). Receptors and ligands are also useful for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. A protein of the present invention (including, without limitation, fragments of receptors and ligands) may themselves be useful as inhibitors of receptor/ligand interactions.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for receptor-ligand activity include without limitation those described in: Current Protocols in Immunology, Ed by J.E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 7.28, Measurement of Cellular Adhesion under static conditions 7.28.1-7.28.22),

Takai et al., Proc. Natl. Acad. Sci. USA 84:6864-6868, 1987;
Bierer et al., J. Exp. Med. 168:1145-1156, 1988; Rosenstein
et al., J. Exp. Med. 169:149-160 1989; Stoltenborg et
al., J. Immunol. Methods 175:59-68, 1994; Stitt et al.,
5 Cell 80:661-670, 1995.

Anti-Inflammatory Activity

Proteins of the present invention may also exhibit
anti-inflammatory activity. The anti-inflammatory activity
may be achieved by providing a stimulus to cells involved in
10 the inflammatory response, by inhibiting or promoting cell-
cell interactions (such as, for example, cell adhesion), by
inhibiting or promoting chemotaxis of cells involved in the
inflammatory process, inhibiting or promoting cell
extravasation, or by stimulating or suppressing production
15 of other factors which more directly inhibit or promote an
inflammatory response. Proteins exhibiting such activities
can be used to treat inflammatory conditions including
chronic or acute conditions), including without limitation
inflammation associated with infection (such as septic shock,
20 sepsis or systemic inflammatory response syndrome (SIRS)),
ischemia-reperfusion injury, endotoxin lethality, arthritis,
complement-mediated hyperacute rejection, nephritis,
cytokine or chemokine-induced lung injury, inflammatory
bowel disease, Crohn's disease or resulting from over
25 production of cytokines such as TNF or IL-1. Proteins of the
invention may also be useful to treat anaphylaxis and
hypersensitivity to an antigenic substance or material.

Tumor Inhibition Activity

In addition to the activities described above for
30 immunological treatment or prevention of tumors, a protein
of the invention may exhibit other anti-tumor activities. A

protein may inhibit tumor growth directly or indirectly (such as, for example, via ADCC). A protein may exhibit its tumor inhibitory activity by acting on tumor tissue or tumor precursor tissue, by inhibiting formation of tissues
5 necessary to support tumor growth (such as, for example, by inhibiting angiogenesis), by causing production of other factors, agents or cell types which inhibit tumor growth, or by suppressing, eliminating or inhibiting factors, agents or cell types which promote tumor growth

10 Other Activities

A protein of the invention may also exhibit one or more of the following additional activities or effects: inhibiting the growth, infection or function of, or killing, infectious agents, including, without limitation, bacteria,
15 viruses, fungi and other parasites; effecting (suppressing or enhancing) bodily characteristics, including, without limitation, height, weight, hair color, eye color, skin, fat to lean ratio or other tissue pigmentation, or organ or body part size or shape (such as, for example, breast
20 augmentation or diminution, change in bone form or shape); effecting biorhythms or circadian cycles or rhythms; effecting the fertility of male or female subjects; effecting the metabolism, catabolism, anabolism, processing, utilization, storage or elimination of dietary fat, lipid,
25 protein, carbohydrate, vitamins, minerals, cofactors or other nutritional factors or component(s); effecting behavioral characteristics, including, without limitation, appetite, libido, stress, cognition (including cognitive disorders), depression (including depressive disorders) and
30 violent behaviors; providing analgesic effects or other pain reducing effects; promoting differentiation and growth of

embryonic stem cells in lineages other than hematopoietic lineages; hormonal or endocrine activity; in the case of enzymes, correcting deficiencies of the enzyme and treating deficiency-related diseases; treatment of hyperproliferative disorders (such as, for example, psoriasis); immunoglobulin-like activity (such as, for example, the ability to bind antigens or complement); and the ability to act as an antigen in a vaccine composition to raise an immune response against such protein or another material or entity which is cross-reactive with such protein.

Examples

The present invention is specifically illustrated in more detail by the following Examples, but Examples are not intended to restrict the present invention. The basic operations with regard to the recombinant DNA and the enzymatic reactions were carried out according to the literature ["Molecular Cloning. A Laboratory Manual", Cold Spring Harbor Laboratory, 1989]. Unless otherwise stated, restrictive enzymes and a variety of modification enzymes to be used were those available from Takara Shuzo. The buffer compositions and the reaction conditions for each of the enzyme reactions were as described in the manufacturer's instructions. The cDNA synthesis was carried out according to the literature [Kato, S. et al., Gene 150: 243-250 (1994)].

(1) Selection of cDNAs Encoding Proteins Having Hydrophobic Domains

The cDNA library of fibrosarcoma cell line HT-1080 (WO98/11217), the cDNA library of osteosarcoma cell line Saos-2 (WO97/33993), the cDNA library of osteosarcoma cell line U-2 OS (WO98/21328), the cDNA library of epidermoid

carcinoma cell line KB (WO98/11217), the cDNA library of tissues of stomach cancer delivered by the operation (WO98/21328), the cDNA library of liver tissue delivered by the operation (WO98/21328), and were used for the cDNA libraries. Full-length cDNA clones were selected from respective libraries and the whole base sequences thereof were determined to construct a homo-protein cDNA bank consisting of the full-length cDNA clones. The hydrophobicity/hydrophilicity profiles were determined for the proteins encoded by the full-length cDNA clones registered in the homo-protein cDNA bank by the Kyte-Doolittle method [Kyte, J. & Doolittle, R. F., J. Mol. Biol. 157: 105-132 (1982)] to examine the presence or absence of a hydrophobic region. Any clone that has a hydrophobic region being putative as a secretory signal or a transmembrane domain in the amino acid sequence of the encoded protein was selected as a clone candidate.

(2) Protein Synthesis by In Vitro Translation

The plasmid vector bearing the cDNA of the present invention was used for in vitro transcription/translation with a T_NT rabbit reticulocyte lysate kit (Promega). In this case, [³⁵S]methionine was added to label the expression product with a radioisotope. Each of the reactions was carried out according to the protocols attached to the kit. Two micrograms of the plasmid was subjected to the reaction at 30°C for 90 minutes in the reaction solution of a total volume of 25 μ l containing 12.5 μ l μ of T_NT rabbit reticulocyte lysate, 0.5 μ l of a buffer solution (attached to the kit), 2 μ l of an amino acid mixture (without methionine), 2 μ l of [³⁵S]methionine (Amersham) (0.37 MBq/ μ l), 0.5 μ l of T7 RNA polymerase, and 20 U of RNasin. Also, an experiment in the presence of a membrane system was carried

out by adding to this reaction system 2.5 μ l of a canine pancreas microsome fraction (Promega). To 3 μ l of the resulting reaction solution was added 2 μ l of the SDS sampling buffer (125 mM Tris-hydrochloric acid buffer, pH 6.8, 120 mM 2-mercaptoethanol, 2% SDS solution, 0.025% bromophenol blue, and 20% glycerol) and the resulting mixture was heated at 95°C for 3 minutes and then subjected to SDS-polyacrylamide gel electrophoresis. The molecular weight of the translation product was determined by carrying out the autoradiography.

(3) Expression by COS7

Escherichia coli cells bearing the expression vector for the protein of the present invention was incubated at 37°C for 2 hours in 2 ml of the 2xYT culture medium containing 100 μ g/ml of ampicillin, the helper phage M13K07 (50 μ l) was added, and the incubation was continued at 37°C overnight. A supernatant separated by centrifugation underwent precipitation with polyethylene glycol to obtain single-stranded phage particles. These particles were suspended in 100 μ l of 1 mM Tris-0.1 mM EDTA, pH 8 (TE).

The cultured cells derived from simian kidney, COS7, were incubated at 37°C in the presence of 5% CO₂ in the Dulbecco's modified Eagle's culture medium (DMEM) containing 10% fetal calf serum. Into a 6-well plate (Nunc, well diameter: 3 cm) were inoculated with 1 x 10⁵ COS7 cells and incubation was carried out at 37°C for 22 hours in the presence of 5% CO₂. After the culture medium was removed, the cell surface was washed with a phosphate buffer solution and then washed again with DMEM containing 50 mM Tris-hydrochloric acid (pH 7.5) (TDMEM). To the resulting cells was added a suspension of 1 μ l of the single-stranded phage suspension, 0.6 ml of the DMEM culture medium, and 3 μ l of

TRANSFECTAM™ (IBF) and the resulting mixture was incubated at 37°C for 3 hours in the presence of 5% CO₂. After the sample solution was removed, the cell surface was washed with TDMEM, 2 ml per well of DMEM containing 10% fetal calf serum was added, and the incubation was carried out at 37°C for 2 days in the presence of 5% CO₂. After the culture medium was replaced by a culture medium containing [³⁵S]cystine or [³⁵S]methionine, the incubation was carried out for one hour. After the culture medium and the cells were separated by centrifugation, proteins in the culture medium fraction and the cell-membrane fraction were subjected to SDS-PAGE.

(4) Clone Examples

<HP01550> (SEQ ID Nos. 1, 11, and 21)

Determination of the whole base sequence of the cDNA insert of clone HP01550 obtained from cDNA library of human stomach cancer revealed the structure consisting of a 65-bp 5'-untranslated region, a 378-bp ORF, and a 67-bp 3'-untranslated region. The ORF codes for a protein consisting of 125 amino acid residues and there existed one putative transmembrane domain. Figure 1 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 15 kDa that was almost identical with the molecular weight of 13,825 predicted from the ORF.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the *Caenorhabditis elegans* hypothetical protein F45G2.c (GenBank Accession No. Z93382). Table 2 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the C.

Table 2

20

25

30

BNSDOCID: <WO_____0005367A2 | >

and a 198-bp 3'-untranslated region. The ORF codes for a protein consisting of 131 amino acid residues and there existed four putative transmembrane domains at the C-terminus. Figure 2 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of a high molecular weight.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to a human OB-R gene-related protein (EMBL Accession No. Y12670). Table 3 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the human OB-R gene-related protein (OB). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 67.9% in the entire region.

Table 3

[illegible]

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA306490) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

<HP10195> (SEQ ID Nos. 3, 13, and 23)

Determination of the whole base sequence of the cDNA insert of clone HP10195 obtained from cDNA library of human fibrosarcoma HT-1080 revealed the structure consisting of a 286-bp 5'-untranslated region, a 729-bp ORF, and a 604-bp 3'-untranslated region. The ORF codes for a protein consisting of 242 amino acid residues and there existed one putative transmembrane domain at the C-terminus. Figure 3 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 32 kDa that was somewhat larger than the molecular weight of 27,300 predicted from the ORF. When expressed in COS7 cells, an expression product of about 21 kDa was observed in the supernatant fraction and the membrane fraction.

The search of the protein data base using the amino acid sequence of the present protein has revealed the registration of sequences that were similar to the Aplysia VAP-33 (SWISS-PROT Accession No. P53173). Table 4 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the Aplysia VAP-33 (AP). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the

present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 46.5% in the entire region.

5

Table 4

	HP	MAKHEQILVLDPPTDLKFKGPFTDVVTNLKLRNPSDRKVCFKVKTAPRRYCVRPNSGI
		*** **.....*****.....**.....*****.....*****
10	AP	MASHEQALILEPAGELRFKGPFTDVVTADLKLSNPTDRRICFKVKTAPKRYCVRPNSGI
	HP	IDPGSTVTVSVMLQPFDDPNEKSKHKFMVQTIFAPPNTSD-MEAVWKEAKPDELMSKL
		..******.....*****.....* .. . * ..**.* ..**.*..*
	AP	LEPKTSIAVAVMLQPFNYDPNEKNKHKFMVQSMYAPDHVVESQELLWKDAPPESLMDTKL
	HP	RCVFEMPENNDKLNMEPSK-----AVPLNASKQDGPMPKP-HSVSLNDTE
15		*****..... * ... ** . *.
	AP	RCVFEMPDGSHQAPASDASRATDAGAHFSESALEDPTVASRKTETQSPKRVGAVGSAGED
	HP	TRKLMEECKRLQGEMMKLSEENRHLRDEGLRLRKVAHSD--KPGSTSTASFRDNVTSPLP
		...* . * . * . * . * . * . * . * . * . * . * . * . * . * . * . *
	AP	VKKLQHELKKAQSEITSLKGENSEQLKDEGIRLRKVAMTDTVSPTPLNPSAPAAAVRAFP
20	HP	SLLVVIAAIFIGFLGKFIL
		...* ..**.* ..**.*..*
	AP	PVVYVVAAILGLIIGKFL

25 Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA447905) in ESTs, but, since they are partial sequences, it can not be judged whether or not

30 any of these sequences codes for the same protein as the protein of the present invention.

<HP10423> (SEQ ID Nos. 4, 14, and 24)

Determination of the whole base sequence of the cDNA insert of clone HP10423 obtained from cDNA library of human osteosarcoma cell line U-2 OS revealed the structure consisting of a 64-bp 5'-untranslated region, a 795-bp ORF, and a 207-bp 3'-untranslated region. The ORF codes for a protein consisting of 264 amino acid residues and there existed a secretory signal at the N-terminus and one putative transmembrane domain at the N-terminus. Figure 4 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 30 kDa that was almost identical with the molecular weight of 29,377 predicted from the ORF. When expressed in COS7 cells, an expression product of about 31 kDa was observed in the membrane fraction.

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. D80116) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

<HP10506> (SEQ ID Nos. 5, 15, and 25)

Determination of the whole base sequence of the cDNA insert of clone HP10506 obtained from cDNA library of human stomach cancer revealed the structure consisting of a 53-bp 5'-untranslated region, a 339-bp ORF, and a 226-bp 3'-untranslated region. The ORF codes for a protein consisting of 112 amino acid residues and there existed one putative transmembrane domain. Figure 5 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-

Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 12 kDa that was almost identical with the molecular weight of 11,821 predicted from the ORF. When expressed in
5 COS7 cells, an expression product of about 13 kDa was observed in the membrane fraction.

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for
10 example, Accession No. AA282544) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

15 <HP10507> (SEQ ID Nos. 6, 16, and 26)

Determination of the whole base sequence of the cDNA insert of clone HP10507 obtained from cDNA library of human stomach cancer revealed the structure consisting of a 412-bp 5'-untranslated region, a 441-bp ORF, and a 168-bp 3'-
20 untranslated region. The ORF codes for a protein consisting of 146 amino acid residues and there existed a secretory signal at the N-terminus and one putative transmembrane domain at the C-terminus. Figure 6 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-
25 Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 19 kDa that was somewhat larger than the molecular weight of 16,347 predicted from the ORF.

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for
30 example, Accession No. AA424759) in ESTs, but, since they

are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

5 <HP10548> (SEQ ID Nos. 7, 17, and 27)

Determination of the whole base sequence of the cDNA insert of clone HP10548 obtained from cDNA library of human stomach cancer revealed the structure consisting of a 330-bp 5'-untranslated region, a 1035-bp ORF, and a 67-bp 3'-untranslated region. The ORF codes for a protein consisting of 344 amino acid residues and there existed four putative transmembrane domains. Figure 7 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of a high molecular weight.

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA143152) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

25 <HP10566> (SEQ ID Nos. 8, 18, and 28)

Determination of the whole base sequence of the cDNA insert of clone HP10566 obtained from cDNA library of the human stomach cancer revealed the structure consisting of a 61-bp 5'-untranslated region, a 294-bp ORF, and a 246-bp 3'-untranslated region. The ORF codes for a protein consisting of 97 amino acid residues and there existed one putative transmembrane domain at the C-terminus. Figure 8 depicts the

hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 12 kDa that was almost identical with the molecular weight of 11,452 predicted from the ORF. When expressed in COS7 cells, an expression product of about 12 kDa was observed in the membrane fraction.

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. W79821) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

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<HP10567> (SEQ ID Nos. 9, 19, and 29)

Determination of the whole base sequence of the cDNA insert of clone HP10567 obtained from cDNA library of the human stomach cancer revealed the structure consisting of a 77-bp 5'-untranslated region, a 375-bp ORF, and a 133-bp 3'-untranslated region. The ORF codes for a protein consisting of 124 amino acid residues and there existed one putative transmembrane domain at the C-terminus. Figure 9 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 14 kDa that was almost identical with the molecular weight of 14,484 predicted from the ORF.

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA428475) in ESTs, but, since they

are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

5 <HP10568> (SEQ ID Nos. 10, 20, and 30)

Determination of the whole base sequence of the cDNA insert of clone HP10568 obtained from cDNA library of the human stomach cancer revealed the structure consisting of a 56-bp 5'-untranslated region, a 984-bp ORF, and a 60-bp 3'-untranslated region. The ORF codes for a protein consisting of 327 amino acid residues and there existed a secretory signal at the N-terminus and one putative transmembrane domain at the C-terminus. Figure 10 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 36.5 kDa that was almost identical with the molecular weight of 34,326 predicted from the ORF. In this case, the addition of a microsome led to the formation of a product of 40 kDa which is considered to have a sugar chain being attached. In addition, there exist in the amino acid sequence of this protein two sites at which N-glycosylation may occur (Asn-Leu-Thr at position 138 and Asn-Leu-Ser at position 206). Application of the (-3,-1) rule, a method for predicting the cleavage site of the secretory signal sequence, allows to expect that the mature protein starts from valine at position 24. When expressed in COS7 cells, an expression product of about 31 kDa was observed in the supernatant fraction and the membrane fraction.

30 The search of the protein data base using the amino acid sequence of the present protein has revealed that the protein was similar to the human cell-surface A33 antigen

(SWISS-PROT Accession No. Q99795). Table 5 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the human cell-surface A33 antigen (A3). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 30.0% in the N-terminal region of 243 residues.

Table 5

	HP	MAELPGPFLLCGALLGFLCLSGLAVEVKVPTEPLSTPLGKTAELTCTYSTSVGDSFAL-EW
	 *... *...*.*** *... . * .*
15	A3	MVGKMWPVLWTLCAVRVTVD AISVETPDVLRASQGKSVTLPCITYHTSTSSREGLIQW
	HP	SFVQPGKPISESHPILYFTNGHLYPTGSKSKRVSL LQNPPTVGVATLKLTDVHPSDTGTY
	 * . * . * . * . * . . * * * *
	A3	DKLL--LTHTERVVIWPF SNKN-YIHGELYKNRVSI SNNAEQSDASITIDQLTMADNGTY
	HP	LCQVNNPPDFYTNGLGLINLTVLVPPSNPLCSQSGQTSVGGSTALRCSSEGAPKPVYNW
20		* * . . * . . . * * * * *
	A3	ECSVSLMSDLEGNTKSRVRL LVLVPPSKPECGIEGETIIGNNIQLTCQSKEGSPTPQYSW
	HP	VRLGTFTPSPGSMVQDEVSGQLILTNLSLTSSGTYRCVATNQMG SASCELTSVTEPS-
		* . . . * * . * . . . * * * *
	A3	KRYNILNQEQP--LAQPASGQPVSLKNISTDTSGYYICTSSNEEGTQFCNITVAVRSPSM
25	HP	-QGRVAGALIGVLLGVLLLSVA AFCLVRFQKERGKKPKETYGGSDLREDAIAPGISEHTC
		. . * . * * .
	A3	NVALYVGIAVGVAALIIIGIIIIYCCCCRGKDDNTEDKEDARPNREAYEEPPEQLRELSR
	HP	MRADSSKGFLERPSSASTVTTTTSKSLPMVV
30	A3	EREEEDDYRQEEQRSTGRES PDHLDQ

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration

of sequences that shared a homology of 90% or more (for example, Accession No. T24595) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

<HP01426> (SEQ ID Nos. 31, 41, and 51)

Determination of the whole base sequence of the cDNA insert of clone HP01426 obtained from cDNA library of human stomach cancer revealed the structure consisting of a 1-bp 5'-untranslated region, a 942-bp ORF, and a 122-bp 3'-untranslated region. The ORF codes for a protein consisting of 313 amino acid residues and there existed a putative secretory signal. Figure 11 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 36 kDa that was almost identical with the molecular weight of 34,955 predicted from the ORF. In this case, the addition of a microsome led to the formation of a product of 38 kDa which is considered to have a sugar chain being attached after secretion. In addition, there exists in the amino acid sequence of this protein one site at which N-glycosylation may occur (Asn-Ser-Ser at position 163). Application of the (-3,-1) rule, a method for predicting the cleavage site of the secretory signal sequence, allows to expect that the mature protein starts from tryptophan at position 17. When expressed in COS7 cells, an expression product of about 39 kDa was observed in the supernatant fraction and the membrane fraction.

The search of the protein data base using the amino acid sequence of the present protein revealed that the

protein was similar to the *Xenopus laevis* cortical granule lectin (EMBL Accession No. X82626). Table 6 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the *X. laevis* cortical granule lectin (XL). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 67.9% in the region other than the N-terminal region.

Table 6

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15 HP MNQLSFLFLIATTRGWSTDEANTYFKEWTCSSSPSLPRSCKEIKDECPSAFDGLYFLRT
    *          **                      *          ***** . * ** * * .
XL MLVHILLLLVTGGLSQSCEPVVIVASKNMVKQLDCDKFRSCKEIKDSNEEAQDGIYTLTS
HP ENGVIIYQTFCDMTSGGGGWTLVASVHENDMRGKCTVGDRWSSQQGSKADYPEGDGNWANY
    . * . ***** . ***** . * ***** . *****
20 XL SDGISYQTFCDMTTNGGGWTLVASVHENNMAGKCTIGDRWSSQQGNRADYPEGDGNWANY
HP NTFGSAEAATSDDYKNPGYYDIQAKDLGIWHVPNKSPMQHWRNSSLRYRTDTGFLQTLG
    ***** . ***** . * . ** . ***** . ***** * * . * . *
XL NTFGSAGGATSDDYKNPGYYDIEAYNLGVWHVPNKTPLSVWRNSSLQRYRTTDGILFKHG
HP HNLFGIYQKYPVKYGEKGCWTDNGPVPVVDYDFGDAQKTASYYSYPGQREFTAGFVQFRV
    *** . * . ***** * . * . * . * . * . * . * . * . * . * . *
25 XL GNLFSLYRIYPVKYGIGSCSKDSGPTVPVVDLGS AKLTASFYSPDFRSQFTPGYIQFRP
HP FNNERAANALCAGMRVTGCNTEHHCIGGGGYFPEAS PQCGDFSGFDWSGYGTHVGYSSS
    . * . * . * * * . * . * . * . * . * . * . * . * . * . * . *
XL INTEKAALALCPGMKMECNVEHVCIGGGGYFPEADPRQCGDFAAYDFNGYGTKKFNSAG
HP REITEAAVLLFYR
30 *****
XL IEITEAAVLLFYL

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Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. R06009) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

<HP02515> (SEQ ID Nos. 32, 42, and 52)

Determination of the whole base sequence of the cDNA insert of clone HP02515 obtained from cDNA library of human osteosarcoma cell line Saos-2 revealed the structure consisting of a 176-bp 5'-untranslated region, a 690-bp ORF, and a 71-bp 3'-untranslated region. The ORF codes for a protein consisting of 229 amino acid residues and there existed a putative secretory signal at N-terminus and one putative transmembrane domain at the C-terminus. Figure 12 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 27 kDa that was almost identical with the molecular weight of 26,000 predicted from the ORF. In this case, the addition of a microsome led to the formation of a product of 25.5 kDa from which the secretory signal is considered to have been cleaved. Application of the (-3,-1) rule, a method for predicting the cleavage site of the secretory signal sequence, allows to expect that the mature protein starts from phenylalanine at position 28.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the human T1/ST2 receptor binding protein (GenBank Accession No. U41804). Table 7 shows the

comparison between amino acid sequences of the human protein of the present invention (HP) and the human T1/ST2 receptor binding protein (T1). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 55.8% in the entire region.

10

Table 7

HP	MGDKIWLPFPVLLLLAALPPVLLPGAAGFTPSLSDSDFFTLPAGQKECFYQPMPLKASLE
	*.... ** .*** . *** . * *****.*****. * .*****
T1	MMAAGAALALALWLL--MPPVEV-GGAGPPPIQDGEFTFLLPAGRKQCFYQSAPANASLE
15 HP	IEYQVLDGAGLDIDFHLASPEGKTLVFEQRKSDGVHTVE-TEVGDMFCFDNTFSTISEK
	.*****.*****.* **.*. * * * *.***** **.*.....*****.*****
T1	TEYQVIGGAGLDVDFTLESPOGVLLVSESARKADGVHTVEPTTEAGDYKLCFDSNFSTISEK
HP	VIFFELILDNMGEQAQEQEDWKYITGTDILDMKLEDILESINSIKSRLSKSGHIQILLR
	..*****.*... ..* *.**.*.*** **.*.....* .. .***
20 T1	LVFFELIFDSL-QDDEEVEGWAEAVEPEEMLDVKMEDIKESIETMRTRLERSIQMLTLRL
HP	AFEARDRNIQESNFDNRVNFWSMVNLVVMVVVSAIQVYMLKSLFEDKRKSRT
	*****.*.*.***** **.*.....*.....*.....*.....*.....*
T1	AFEARDRNLQEGNLERVNFWSAVNVAVLLLVAVLQVCTLKRFFQDKRPVPT

25

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA381943) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

30

<HP02575> (SEQ ID Nos. 33, 43, and 53)

Determination of the whole base sequence of the cDNA insert of clone HP02575 obtained from cDNA library of human osteosarcome cell line Saos-2 revealed the structure consisting of a 55-bp 5'-untranslated region, a 1404-bp ORF, and a 219-bp 3'-untranslated region. The ORF codes for a protein consisting of 467 amino acid residues and there existed a putative secretory signal at the N-terminus. Figure 13 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 52 kDa that was almost identical with the molecular weight of 54,065 predicted from the ORF. In this case, the addition of a microsome led to the formation of a product of 57 kDa which is considered to have a sugar chain being attached afetr secretion. In addition, there exist in the amino acid sequence of this protein three sites at which N-glycosylation may occur (Asn-Arg-Thr at position 171, Asn-Ser-Thr at position 239 and Asn-Asp-Thr at position 377). Application of the (-3,-1) rule, a method for predicting the cleavage site of the secretory signal sequence, allows to expect that the mature protein starts from histidine at position 29. When expressed in COS7 cells, an expression product of about 55 kDa was observed in the supernatant fraction.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the human α -L-fucosidase (SWISS-PROT Accession No. P04066). Table 8 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the human α -L-fucosidase (FC). Therein,

Table 8

10 HP MRPQELPRLAFPLLLLLLLLLLPPPPC-PAHSATRFDPTWESLDRQLPAWFDQAKFGIFI
 *****.* .. . *... *...* ***.*.....*****.* **
 FC MRSRPAGPALLLLLLFLGAAESVRRRAQPPRRYTPDWPSLDSRPLPAWFDEAKFGVFI
 HP HWGVFSVPSFGSEWFWWYWQKEKIPKYVEFMKDNYPSPFKYEDFGPLFTAKFFNANQWAD
 *****.*.....** * *. * *...*****.*.*.*** ***.***...***
 FC HWGVFSVPAWGSEWFWWHWQGEGRPOYQRFMRDNYPGFSYADFGPQFTARFFHPEEWAD
 15 HP IFQASGAKYIVLTSKHHEGFTLWGSEYSWNWNAIDEGPKRDIVKELEVAIRNRTDLRFGL
 .*....*.....* * *****. * ***.*.* *...*.***. *...***
 FC LFQAAGAKYVVLTTKHHEGFTNWSPSVSWNWSKDVGPHRDVLVGELGTALRKR-NIRYGL
 HP YYSLEWFHPLFLEDESSSFHKRQFPVSKTLPELYELVNNYQPEVLWSDGDGGAPDQYWN
 *...*****.* *.....*...* *...*****.*.*...*****. . ** ***
 20 FC YHSLEWFHPLYLLDKKNGFKTQHFVSAKTMPELYDLVNSYKPDLIWSDGEWECPDITYWN
 HP STGFLAWLYNESPVRGTVVTNDRWGAGSICKHGGFYTCSDRYNPGHLLPHKWENCMTIDK
 .*...**.*.....*****... *...*.***.*...* * *...* * .***
 FC STNFLSWLYNDSPVKDEVVVNDRWGQNCCHGGYNCEDKFKPQSLPDHKWEMCTSIDK
 HP LSWGYYRREAGISDYLTIEELVKQLVETVSCGGNLLMNIGPTLDGTISVVFEERLRQMGSW
 25 *****. ** * . *...***.*...*** *...***** ** * .*...* ..*.
 FC FSWGYYRDMALSDVTEESEIISELVQTVSLGGNYLLNIGPTKDGILVPIFQERLLAVGKW
 HP LKVNGEAIYETHTWRSQNDTVTPDVWYTSKPKEKLVYAIFLKWPTSGQLFLGHPKAILGA
 *...*****...** * .. *...***** .. *****.*...* * *..* ..
 FC LSINGEAIYASKPWRVQWEKNTTSVWYTSKGS--VYAIFLHWPENGVLNLESPITT-ST
 30 HP TEVKLLGHGQPLNWISLEQNGIMVELPQLTIHQMPCKWGWALALTNVI
 *...** *.* . *...*****. ..* ...*.. ***.
 FC TKITMLGIQGDLEKSTDPDKGLFISLPQLPPSAVPAEFAWTIKLTGVK

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. N28668) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

10 <HP10357> (SEQ ID Nos. 34, 44, and 54)

Determination of the whole base sequence of the cDNA insert of clone HP10357 obtained from cDNA library of human stomach cancer revealed the structure consisting of a 113-bp 5'-untranslated region, a 300-bp ORF, and a 54-bp 3'-untranslated region. The ORF codes for a protein consisting of 99 amino acid residues and there existed two putative transmembrane domains. Figure 14 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 11 kDa that was almost identical with the molecular weight of 10,923 predicted from the ORF.

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA477156) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

30 <HP10447> (SEQ ID Nos. 35, 45, and 55)

Determination of the whole base sequence of the cDNA

insert of clone HP10447 obtained from cDNA library of human liver revealed the structure consisting of a 271-bp 5'-untranslated region, a 570-bp ORF, and a 34-bp 3'-untranslated region. The ORF codes for a protein consisting of 189 amino acid residues and there existed five putative transmembrane domains. Figure 15 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of high molecular weight.

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA296976) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

<HP10477> (SEQ ID Nos. 36, 46, and 56)

Determination of the whole base sequence of the cDNA insert of clone HP10477 obtained from cDNA library of human liver revealed the structure consisting of a 149-bp 5'-untranslated region, a 1092-bp ORF, and a 15-bp 3'-untranslated region. The ORF codes for a protein consisting of 363 amino acid residues and there existed one putative transmembrane domain at the N-terminus. Figure 16 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 40 kDa that was almost identical with the molecular weight of 39,884 predicted from the ORF.

The search of the protein data base using the amino

acid sequence of the present protein revealed that the protein was similar to the human peptidoglycan recognition protein (GenBank Accession No. AF076483). Table 9 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the human peptidoglycan recognition protein (PG). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 54.8% in the entire region.

Table 9

15	HP	MVDSLLAVTLAGNLGLTFLRGSQTQSHPDLGTEGCWDQLSAPRTFTLLDPKASLLTKAFL
	HP	NGALDGVILGDYLSRTPEPRPSLSHLLSQYYGAGVARDPGFRSNFRRQNGAALTSASILA
	HP	QQVWGTLVLLQRLEPVHLQLQCMSQEQLAQVAANATKEFTEAFLGCPAHPRCRWGAAPY
		.. ** * * .
	PG	MSRRSMLLAWALPSLLRLGAAQETEDPACCSPIVPRNEWKALA-
20	HP	RGRP KLLQLPLGFLYVHHTYVPAPPCTDFTRCAANMRSMQRYHQDTQGWGDIGYSFVVGS
	 * *** .. * ***...*...*...*...*...*...*
	PG	SECAQHLSLPLRYVVVSHT--AGSSCNTPASCQQQARNVQHYHMKTLGWCDVGYNFLIGE
	HP	DGYVYEGRGWHWVGAHTLGH-NSRGFGVAIVGNMTAALPTEAALRTVRDTLPSCAVRAGL
		** *****.....**...*...*...*...*...*...*
25	PG	DGLVYEGRGWNFTGAHSGHLWNPMSIGISFMGNMMDRVPTPQAIRAAQGLL-ACGVAQGA
	HP	LRPDYALLGHRQLVRTDCPGDALFDLLRTWPHFTATVKPRPARSVSKRSRREPPPTLPA
	* ***.. ***...*...*...*...*
	PG	LRSNYVLKGHRDVQRTLSPGNQLYHLIQNWPHYRSP

30

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration

of sequences that shared a homology of 90% or more (for example, Accession No. AA424759) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

<HP10513> (SEQ ID Nos. 37, 47, and 57)

Determination of the whole base sequence of the cDNA insert of clone HP10513 obtained from cDNA library of human stomach cancer revealed the structure consisting of a 134-bp 5'-untranslated region, a 750-bp ORF, and a 0-bp 3'-untranslated region. The ORF codes for a protein consisting of 249 amino acid residues and there existed one putative transmembrane domain at the N-terminus. Figure 17 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 29 kDa that was almost identical with the molecular weight of 27,373 predicted from the ORF.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the human hypothetical protein KIAA0512 (GenBank Accession No. AB011084). Table 10 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the human hypothetical protein KIAA0512 (KI). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 31.6% in the C-terminal region of 196 amino acid residues.

Table 10

5 HP MGGPRGAGWVAAGLLLGAGACYCIYRLTRGRRR

KI RGRGRRPVAMQKRPFPEIDEILGVRDLRKVLALLQKSDDPFIQQVALLTSLNNANYSCN

HP DRELGIRSSKSAEDLTDGSYDDVLNAEQLQKLLYLLESTEDPVIIERALITLGNNAAFSV

* * . * * . * *

10 KI QETIRKLGGLPPIANMINKTDPHIKEKALMAMNNLSENYENQGRQVYMNKVMDDIMASN

HP NQAIIRELGGIPIVANKINHSNQSIKEKALNALNNLSVNVENQIKIKVQVLKLLLNLSN

.. .. * ... * ****..**.* *..**

KI LNSAVQVVGLKFLTNTITNDYQHLLVNSIANF--FRLLSQGGGKIKVEILKILSNFAEN

HP PAMTEGLLRAQVDSSFLSLYDSHVAKEILLRVLTFLQNIKNCLKIEGHLAVQPTFTEGSL

. . ****. . ** ****.*.*.....* . * . * ****

15 KI PDMLKLLSTQVPASFSSLYNSYVESEILINALTLFEIYDNLRAE--VFNYREFNKGSL

HP FFL-LHGEECAQKIRALVDHHDAAEVKEKVVTIIPKI

. .. *..*****..** ** **..*.*

KI FYLCTTSGVCVKKIRALANHHDLLVKVKVIKLVNKF

20

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. N92228) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

<HP10540> (SEQ ID Nos. 38, 48, and 58)

30

Determination of the whole base sequence of the cDNA insert of clone HP10540 obtained from cDNA library of human osteosarcoma cell line Saos-2 revealed the structure

consisting of a 47-bp 5'-untranslated region, a 297-bp ORF, and a 245-bp 3'-untranslated region. The ORF codes for a protein consisting of 98 amino acid residues and there existed two putative transmembrane domains. Figure 18 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of high molecular weight.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the *Caenorhabditis elegans* hypothetical protein CEF49C12.12 (GenBank Accession No. Z68227). Table 11 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the *C. elegans* hypothetical protein CEF49C12.12 (CE). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 36.1% in the entire region.

Table 11

25	HP M-ASLLCCGPKLAACGIVLSAWGVIMLIMLGIFNVHSAVLIEDVPFTEKDFENGPNQNIY
	* *** * * * * * * * * * * *
	CE MGKICPLMGPKMSAFCMVMSVWGVIFLGLLGVFYIQAVTLFPDLHF-EGHGKVPSSVID
	HP NLYEQVSYNCFIAAGLYLLGGFSFCQVRLNKRKEYMVR
	* * * * * * * * * *
30	CE AKYNEKATQCWIAAGLYAVTLIAVFWQ---NKYNTAQIF

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA420715) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

10 <HP10557> (SEQ ID Nos. 39, 49, and 59)

Determination of the whole base sequence of the cDNA insert of clone HP10557 obtained from cDNA library of human stomach cancer revealed the structure consisting of a 24-bp 5'-untranslated region, a 519-bp ORF, and a 130-bp 3'-untranslated region. The ORF codes for a protein consisting of 172 amino acid residues and there existed a putative secretory signal at the N-terminus. Figure 19 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 32 kDa that was larger than the molecular weight of 18,844 predicted from the ORF. In this case, the addition of a microsome led to the formation of a product of 39 kDa which is considered to have been subjected to some modification after secretion. In addition, there exist in the amino acid sequence of this protein no site at which N-glycosylation may occur. Application of the (-3,-1) rule, a method for predicting the cleavage site of the secretory signal sequence, allows to expect that the mature protein starts from glycine at position 32. When expressed in COS7 cells, an expression product of about 20 kDa was observed in the supernatant fraction and the membrane fraction.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the human progesterone binding protein (EMBL Accession No. AJ002030). Table 12 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the human progesterone binding protein (PG). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 30.5% in the C-terminal region of 151 amino acid residues.

Table 12

15	HP	MVGPA
	<hr/>	
	PG MAAGDGDVKGTLGSGSESSNDGGSESPGDAGAAEGGGWAAAALALLTGGGEMLLNVAL	
	HP RRRLRPLAALALVLALAPGLPTARAGQTPRPAERGPV--RLFTEELARYGGEEDQPI	
20	** **.. *.. * *.. *.. *.. *.. *	
	PG VALVLLGAYRLWVRWGRRGLGAGAGAGEESPATSLPRMKKRDFSLEQLRQYDG--SRNPRI	
	HP YLAVKGVVFDVTSGKEFYGRGAPYNALTGKDSTRGVAKMSLDPADLTHDTTGLTAKELEA	
	.* **.*.....**.. ..*.....*.....*.....*.....*.....*	
	PG LLAVNGKVFDVTGSKFYGPAGPYGIFAGRDA SRGLATFCLDKDALRDEYDDLSDLNAVQ	
25	HP LDEV--FTKVYKAKYPIVGYTARRILNEDGSPNLDFKPEDQPHFDIKDEF	
	...**. ** ..*.. *.. *.. *.. *.. *.. *.. *	
	PG MESVREWEMQFKEY---DYVG--RLKPGEEPS-EYTDEEDTKDHNKQD	
	<hr/>	

30 Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for

example, Accession No. AA101709) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

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<HP10563> (SEQ ID Nos. 40, 50, and 60)

Determination of the whole base sequence of the cDNA insert of clone HP10563 obtained from cDNA library of human osteosarcoma cell line Saos-2 revealed the structure consisting of a 126-bp 5'-untranslated region, a 363-bp ORF, and a 936-bp 3'-untranslated region. The ORF codes for a protein consisting of 120 amino acid residues and there existed two putative transmembrane domains. Figure 20 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 18.5 kDa that was larger than the molecular weight of 13,180 predicted from the ORF.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the Arabidopsis thaliana hypothetical protein F27F23.15 (GenBank Accession No. AC003058). Table 13 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the A. thaliana hypothetical protein F27F23.15 (AT). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 35.5% in the entire region.

Table 13

HP MMPSRTNLATGIPSSKVKYSRLSSTDDGYIDLQFKKTPPKIPYKAIALATVLFLLIGAFLLI
 * *.**..*...*..*
 5 AT MAYVDHAFSISDEDLMIGTSY-TVSNRPPVKEISLAVGLLVFGTLGI
 HP IIGSLLLSGYISKGGADRAVPVLIIGILVFLPGFYHLRIAYYASKGYRGYSYDDIPDFDD
 ..* * * *.**..*...*..*
 AT VLGFFMAYNRVG-GDRGHGIFIVLGCLLFIPGFYYTRIAYYAYKGYKGFSFSNIPSV

10

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA083574) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

15

<HP01467> (SEQ ID Nos. 61, 71, and 81)

20

Determination of the whole base sequence of the cDNA insert of clone HP01467 obtained from cDNA library of human fibrosarcoma cell line HT-1080 revealed the structure consisting of a 65-bp 5'-untranslated region, a 924-bp ORF, and a 447-bp 3'-untranslated region. The ORF codes for a protein consisting of 307 amino acid residues and there existed three putative transmembrane domains. Figure 21 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of high molecular weight.

25

30

The search of the protein data base using the amino

acid sequence of the present protein revealed that the protein was similar to the rat Sec22 homologue (GenBank Accession No. U42209). Table 14 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the rat Sec22 homologue (RN). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 94.6% in the N-terminal region of 241 amino acid residues. The protein of the present invention was longer by 53 amino acids at the C-terminus than the rat Sec22 homologue.

Table 14

	HP	MSMILSASVIRVRDGLPLSASTDYEQSTGMQECRKYFKMLSRKLAQLPDRCTLKTGHYNI
		*****.*****.***.*.*****.*****.***
	RN	MSMILSASVVRVRDGLPLSASTDCEQSAGVQECRKYFKMLSRKLAQFPDRCTLKTGRHNI
20	HP	NFISSLGVSMMMLCTENYPNVLAFLDELQKEFITTYNMMKTNTAVRPYCFIEFDNFIQ

	RN	NFISSLGVSMMMLCTENYPNVLAFLDELQKEFITTYNMMKTNTAVRPYCFIEFDNFIQ
	HP	RTKQRYNNPRSLSTKINLSDMQTEIKLRPPYQISMCELGSANGVTSAFSVDCKGAGKISS
		*****.*****
25	RN	RTKQRYNNPRSLSTKINLSDMQMEIKLRPPYQIPMCELGSANGVTSAFSVDCKGAGKISS
	HP	AHQRLPATLSGIVGFILSLLCGALNLIRGFHAIESLLQSDGDDFNIIAFLGTAACLY
		*****.*****.***.*.*****
	RN	AHQRLPATLSGIVAFILSLLCGALNLIRGFHAIESLLQSDGEDFSYMI AFLGTAACLY
	HP	QCYLLVYYTGWRNVKSFLTFGLICLCNMYLYELRNWQLFFHVTGAFVTLQIWL RQAQG
30		*
	RN	QMICLCLOGRKERT

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA421925) in ESTs, but, since they
5 are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

<HP01956> (SEQ ID Nos. 62, 72, and 82)

10 Determination of the whole base sequence of the cDNA insert of clone HP01956 obtained from cDNA library of human liver revealed the structure consisting of a 86-bp 5'-untranslated region, a 552-bp ORF, and a 359-bp 3'-untranslated region. The ORF codes for a protein consisting
15 of 183 amino acid residues and there existed one putative transmembrane domain. Figure 22 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product
20 of 20.5 kDa that was almost identical with the molecular weight of 20,073 predicted from the ORF.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the yeast hypothetical protein 21.5
25 kDa (SWISS-PROT Accession No. P53073). Table 15 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the yeast hypothetical protein 21.5 kDa (SC). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that
30 of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology

of 34.3% in the C-terminal region of 108 amino acid residues.

Table 15

5 HP MTAQGGLVANRGRRFKWAIELSGPGGGSRGRSDRGSGQGDSLYPVGYLDKQVPDTS

SC MSEQEPYEWAKHLLDTKYIEKYNIQNSNTLPSPPGFEGNSSKGNVTRKQDQDQTSQTSLA

HP VQETDRILVEKRCWDIALGPLKQIPMNLFIMYMAGNTISIFPTMMVCMMAWRPIQALMAI

 .* .. *.*.* * * *.*.*. *.*.*. *.*.* . * . *.*.*.*.

10 SC QKNQITVLQVQKAWQIALQPAKSIPMNIFMSYMSGTSLQIIPIMTALMLLSGPIKAIFST

HP SATFK--MLESSSQKFLQGLVYLIGNLMGLALAV-Y-KCQSMGLLPTHASDWLAFIEPPE

 ...*** . *. * . . . * * .*.*.*.*. .***.

SC RSAFKPVLGNKATQSQVQTAMFMYIVFQGVLMYIGYRKLNSMGLIPNAKGDWLPWERIAH

HP RMEFSGGGLLL

15

SC YNNGLQWFSD

20 Furthermore, the search of the GenBank using the base
 sequences of the present cDNA has revealed the registration
 of sequences that shared a homology of 90% or more (for
 example, Accession No. AA159753) in ESTs, but, since they
 are partial sequences, it can not be judged whether or not
 any of these sequences codes for the same protein as the
 25 protein of the present invention.

<HP02545> (SEQ ID Nos. 63, 73, and 83)

30 Determination of the whole base sequence of the cDNA
 insert of clone HP02545 obtained from cDNA library of human
 osteosarcoma cell line Saos-2 revealed the structure
 consisting of a 133-bp 5'-untranslated region, a 984-bp ORF,
 and a 636-bp 3'-untranslated region. The ORF codes for a

protein consisting of 327 amino acid residues and there existed a putative secretory signal at the N-terminus and one putative transmembrane domain at the C-terminus. Figure 23 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the rat embigin (EMBL Accession No. AJ009698). Table 16 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the rat embigin (RN). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 65.4% in the entire region.

HP MRALPGLLEARARTPRLLLLLQCLLAARPSADGPSAPFTSPPLREEIMAN--NFSLE
 ** . ** . *.. **********
 5 RN MRSHTGLRALVAPGCSLLLL-YLLAATRPDRAVGDPADSFTSLPVREEMMAKYANLSLE
 HP SHNISLTEHSSMPVEKNITLERPSNVNLTCQFTTSGDLNAVNVTWKKDGEQLE--NNYLV
 ..*****.....*.*****.....**.....* ..*****.. ** ...
 RN TYNISLTEQTRVS-EQNITLERPSHLECTFTATEDVMSMNVTWKKDDALLETTDGFNT
 HP SATGSTLYTQYRFTIINSKQMGSYSCTFREEKEQRGTNFVKPELHGKNKPLISYVG DST
 10 . *.****.*****.*****.*****. ** *****.....*****.*****
 RN TKMGDTLYSQYRFTVFNSKQMGKYS CFLGEE--LRGTFNIRVPKVHGNKPLITYVG DST
 HP VLTCKCQNCFP LNWTWYSSNGSVKVPVGVQM-NKYVINGTYANETKLKITQLLEEDGESY
 . *.**.*****.***...*...*. *. ****.*****.....*****.*
 RN VLKCECQCNCLPLNWTWYMSGTAQVPIDVHVNDKFDINGSYANETKLKVHLLLEEDGGSY
 15 HP WCRAFQLGESEEHIELVLVLSYLVP LKPFLVIVA EVILLVATILLCEKYTQKKKKHSDEG
 **** *.*****.*****.*****.*****.*****.*****.....*.
 RN WCRAAFPLGESEEHIKLVLSFMVPLKPFLAIIEVILLVAIILLCEVYTQKKKN DPDDG
 HP KEFEQIEQLKSDDSNGIENNVPRHRKNESLGQ
 *****.....**..*..
 20 RN KEFEQIEQLKSDDSNGIENNVPRYRKTD SGDO

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA312629) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

<HP02551> (SEO ID Nos. 64, 74, and 84)

Determination of the whole base sequence of the cDNA insert of clone HP02551 obtained from cDNA library of human

osteosarcoma cell line Saos-2 revealed the structure consisting of a 61-bp 5'-untranslated region, a 672-bp ORF, and a 384-bp 3'-untranslated region. The ORF codes for a protein consisting of 223 amino acid residues and there existed a putative secretory signal at the N-terminus. Figure 24 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 27 kDa that was somewhat larger than the molecular weight of 24,555 predicted from the ORF. In this case, the addition of a microsome led to the formation of a product of 26 kDa from which the secretory signal is considered to have been cleaved. Application of the (-3,-1) rule, a method for predicting the cleavage site of the secretory signal sequence, allows to expect that the mature protein starts from glutamine at position 20.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the mouse FGF binding protein (GenBank Accession No. U49641). Table 17 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the mouse FGF binding protein (MM). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 21.2% in the entire region other than the N-terminal region. In particular, all the eight cysteine residues contained in the both proteins were conserved.

Table 17

	HP	MKFVPCLLLVTLSCLGTLGQAPRQKQGST
		..**.. . *
5	MM	MRLHSLILLSFLLLATQAFSEKVRKRAKNAPHSTAEEGVEGSAPSLGKAQNKQRSRTSKS
	HP	GEEFHFQTGGRDSCMRPSSLGQGAGEVWLRVDCRNTDQTYWCEYRGQPSMCQAFADPK
		.. * * .. * * . * . * . * . * . * . * .
	MM	LTHGKFVTKDQATC---RWAVTEEEQGISLKVQCTQADQEFSCVFAGDPTDCLKHDKD-Q
	HP	SYWNQALQELRRLHHACQGA-PVLRPSVCREAGPQAHMQQVTSSLKGSPEPNQQPEAGTP
10		** . * * . * . * . * . * . . . *
	MM	IYWKQVARTLRKQKNICRDAKSVLKTRVCRKRFPESNLKLVNPNARGNTKPRKEKAEVSA
	HP	SLRPKATVKLTEATQLGKDSMEELGKAKPTTRPTAKPTQPGPRPGGNEEAKKKAWEHCWK
		. . * * . . . * . * . * . . . * . . . * . * .
	MM	REHNKVQEAVSTEPNRIKEDI-TLNPAATQTM-TIRDPECLEDPDVLNQ-RKTALEFCGE
15	HP	PFQALCAFLISFFRG
		.. . * . *
	MM	SWSSICTFFLNMLQATSC

20 Furthermore, the search of the GenBank using the base
sequences of the present cDNA has revealed the registration
of sequences that shared a homology of 90% or more (for
example, Accession No. AA317400) in ESTs, but, since they
are partial sequences, it can not be judged whether or not
25 any of these sequences codes for the same protein as the
protein of the present invention.

<HP02631> (SEQ ID Nos. 65, 75, and 85)

30 Determination of the whole base sequence of the cDNA
insert of clone HP02631 obtained from cDNA library of human
osteosarcoma cell line Saos-2 revealed the structure
consisting of a 42-bp 5'-untranslated region, a 147-bp ORF,

and a 1191-bp 3'-untranslated region. The ORF codes for a protein consisting of 48 amino acid residues and there existed a putative secretory signal at the N-terminus. Figure 25 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 10 kDa or less.

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA156969) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

15

<HP02632> (SEQ ID Nos. 66, 76, and 86)

Determination of the whole base sequence of the cDNA insert of clone HP02632 obtained from cDNA library of human fibrosarcoma cell line HT-1080 revealed the structure consisting of a 50-bp 5'-untranslated region, a 1116-bp ORF, and a 337-bp 3'-untranslated region. The ORF codes for a protein consisting of 371 amino acid residues and there existed eight putative transmembrane domains. Figure 26 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of high molecular weight.

25

30

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the *Caenorhabditis elegans* hypothetical protein CELC2H12 (GenBank Accession No. U23169). Table 18 shows the comparison between amino acid sequences

5

Table 18

HP MAWTKYQLFLAGLMLVTGSINTLSAKWADNFM AEGCGGSKEHSFQHPFLQAVGMFLGEFS
 *.*****.*****.....* . *.*****. **.***
 CE MVAFAVIISVMVVTGSLNTICAKWADSIKAD-----GVFPNHPFLQATCMFFGEFL
 HP CLAAFYL-----LRCRAAGQSDS-----SVDPQQPFNPLLFLPPALCDMTGTSL
 ..*.* * ..*.* * . . ***.*****. ***.
 CE CLVVFFLIFGYKRYVWNRANVQGESGSVTEITSEEKPTLPPFNPFLLFFPPALCDILGTSI
 HP MYVALNMTSASSFQMLRGAVIIFTGLFSVAFLGRRLVLSQWL GILATIAGLVVUGLADLL
 ..*.*.***.*****.*****.*****. . . *.*.*. . . ***.*.*.*.
 CE MYIGLNLTTASSFQMLRGAVIIFTGLLSVGMLNAQIKPKWFGMLFVMLGLVIVGVTDIY
 HP SKHDSQHKLSEVITGDLLIIMAQIIVAIQM VLEEKFVYKHNHPLRAVGTEGLFGFVILS
 ..* . . .***.***.*****.***** *.*.. *.*.*.* *** *****.*.*
 CE YDDPLDDKNAIITGNLLIVMAQIIVAIQM VYEQKYLT KYDVPALFAVGLEGLFGMVTL
 HP LLLVPMYYIPAG-SFSGNPRGTLEDALDAFCQVGQQPLIAVALLGNISSIAFFNFAGISV
 ..*.*.*****. .**.*.* * ****..* * **.*.* *.. *****.*.*
 CE ILMIPFYYIHVPRTFSTNPEGRLEDVFYAWKEITEEPTIALALSGTVVSI AFFNFAGVSV
 HP TKELSATTRMVLDSLRTVVIWALSLALGWEAFHALQILGFLILLIGTALYNGLHRPLLGR
 *****.*****.*****.***** * * * * * . ** * . * . .
 CE TKELSATTRMVLDSVRTLVIWVVSIP LFHEKFIAIQLSGFAMLILGTLIYNDILIGPWR
 HP LSRGRPLAESEQERLLGGTRTPINDAS
 CE RNILPNLSSHANCARCWLCICGGDSELIEYEQEDQEHLMEA

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. N50907) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

<HP10488> (SEQ ID Nos. 67, 77, and 87)

Determination of the whole base sequence of the cDNA insert of clone HP10488 obtained from cDNA library of human liver revealed the structure consisting of a 39-bp 5'-untranslated region, a 273-bp ORF, and a 421-bp 3'-untranslated region. The ORF codes for a protein consisting of 90 amino acid residues and there existed one putative transmembrane domain at the N-terminus. Figure 27 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 10 kDa that was almost identical with the molecular weight of 10,151 predicted from the ORF. When expressed in COS7 cells, an expression product of about 6 kDa was observed in the membrane fraction.

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. H73534) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

<HP10538> (SEQ ID Nos. 68, 78, and 88)

Determination of the whole base sequence of the cDNA insert of clone HP10538 obtained from cDNA library of human osteosarcoma cell line Saos-2 revealed the structure consisting of a 357-bp 5'-untranslated region, a 1500-bp ORF, and a 1911-bp 3'-untranslated region. The ORF codes for a protein consisting of 499 amino acid residues and there existed at least four putative transmembrane domains. Figure 28 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of high molecular weight.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the mouse pore-forming K⁺ channel subunit (GenBank Accession No. AF056492). Table 19 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the mouse pore-forming K⁺ channel subunit (MM). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 32.4% in the N-terminal region of 241 amino acid residues.

20 Furthermore, the search of the GenBank using the base
sequences of the present cDNA has revealed the registration
of sequences that shared a homology of 90% or more (for
example, Accession No. R25184) in ESTs, but, since they are
partial sequences, it can not be judged whether or not any
25 of these sequences codes for the same protein as the protein
of the present invention.

Determination of the whole base sequence of the cDNA
30 insert of clone HP10542 obtained from cDNA library of human
stomach cancer revealed the structure consisting of a 23-bp
5'-untranslated region, a 321-bp ORF, and a 426-bp 3'-

untranslated region. The ORF codes for a protein consisting of 106 amino acid residues and there existed one putative transmembrane domain. Figure 29 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 12 kDa that was almost identical with the molecular weight of 11,724 predicted from the ORF. When expressed in COS7 cells, an expression product of about 13 kDa was observed in the membrane fraction.

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA029683) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

<HP10571> (SEQ ID Nos. 70, 80, and 90)

Determination of the whole base sequence of the cDNA insert of clone HP10571 obtained from cDNA library of human stomach cancer revealed the structure consisting of a 95-bp 5'-untranslated region, a 459-bp ORF, and a 675-bp 3'-untranslated region. The ORF codes for a protein consisting of 152 amino acid residues and there existed one putative transmembrane domain. Figure 30 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 20 kDa that was larger than the molecular weight of 17,062 predicted from the ORF. In this case, the addition of a microsome led to the formation of a product of 23 kDa

which is considered to have a sugar chain being attached after secretion. In addition, there exists in the amino acid sequence of this protein one site at which N-glycosylation may occur (Asn-Ile-Thr at position 10).

5 Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA105822) in ESTs, but, since they are partial sequences, it can not be judged whether or not
10 any of these sequences codes for the same protein as the protein of the present invention.

<HP01470> (SEQ ID Nos. 91, 101, and 111)

15 Determination of the whole base sequence of the cDNA insert of clone HP01470 obtained from cDNA library of human stomach cancer revealed the structure consisting of a 157-bp 5'-untranslated region, a 1077-bp ORF, and a 385-bp 3'-untranslated region. The ORF codes for a protein consisting of 358 amino acid residues and there existed one putative
20 transmembrane domain. Figure 31 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 43 kDa that was somewhat larger than the molecular weight
25 of 40,489 predicted from the ORF. In this case, the addition of a microsome led to the formation of a product of 40 kDa from which the secretory signal is considered to have been cleaved and a product of 43.5 kDa which is considered to have been subjected to some modification. Application of the
30 (-3,-1) rule, a method for predicting the cleavage site of the secretory signal sequence, allows to expect that the mature protein starts from glycine at position 23. When

expressed in COS7 cells, an expression product of about 44 kDa was observed in the supernatant fraction.

5 The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the *Caenorhabditis elegans* hypothetical protein 39.9 kDa (SWISS-PROT Accession No. Q10005). Table 20 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the *C. elegans* hypothetical protein 39.9 kDa (CE).
10 Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 58.9% in the entire
15 region.

Table 20

HP MAPQNLSTFCLLLLYLIGAVIAGRDFYKILGVPRASIKDIKKAYRKLALQLHPDRNPDD
 *.. * *****...*. ..***** .*****.**

5 CE MRILNVSLVLAASSLVAFVECGRDFYKILGVAKNANANQIKKAYRKLAKELHPDRNQDD
 HP PQAQEKFDLGAAYEVLSDSEKRRQYDTYGEEGL--KDGHQSSHGDIFSHFFGDFGFMFG
 *.*****.*****.*** ** .*****. ..* .. * ** ***** *

CE EMANEKFQDLSSAYEVLSDKEKRAMYDRHGEEGVAKMGGGGGGGGHDPFSSFFGDF-FG-G
 HP GTPRQQDRNIPRGSDIIVDLEVTLEEVYAGNFVEVVRNKPVARQAPGKRKCNCRQEMRTT

10 *. . . .*.*.*.*** *****.*.****. *.*. * .*.*.*****.*****.
 CE GGGHGGEEGTPKGADVTIDLFVTLEEVYNGHFVEIKRKKAVYKQTSQTRQCNCRHEMRTE
 HP QLGPGRFQMTQEVVCDPCPNVKLVNEERTLEVEIEPGVRDGMIEYPPFIGEGEPHVDGEPGD
 *.***** * *****.*****.*.*****. * . * . * *****.*****

CE QMGQGRFQMFQVKVCDECPNVKLVQENKVLEVEVEVGADNGHQQIFHGEGEPHIEGDPGD
 15 HP LRFRIKVVKHPIFERRGDDLYTNVTISLVESLVGFEMDITHLDGHKVVHISRDKITRPGAK
 *.***.*** *****.*****.*** *****.*****.***.*****.
 CE LKFKIRIQKHPRFERKGDDLYTNVTISLQDALNGFEMEIQHLDGHIVKVQRDKVTWPGAR
 HP LWKKGEGLPNFDNNNIKGSIIITFDVDFPKEQLTEEAREGIKQLLKQGSVQ-KVYNGLQG
 *.***.***.***** ** *.*****.*****.*****. * ..*.***.***.*****

20 CE LRKKDEGMPSLEDNNKKGMLVVTDFVEFPKTELSDEQKAQIIEILOQNTVKPKAYNGL

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA282838) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

30 <HP002419> (SEQ ID Nos. 92, 102, and 112)

Determination of the whole base sequence of the cDNA insert of clone HP02419 obtained from cDNA library of human stomach cancer revealed the structure consisting of a 253-bp

5'-untranslated region, a 681-bp ORF, and a 1120-bp 3'-untranslated region. The ORF codes for a protein consisting of 226 amino acid residues and there existed four putative transmembrane domains. Figure 32 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of high molecular weight.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the human hypothetical protein KIAA0108 (SWISS-PROT Accession No. Q15012). Table 21 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the human hypothetical protein KIAA0108 (KI). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 43.9% in the entire region.

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA173214) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

Determination of the whole base sequence of the cDNA insert of clone HP02631 obtained from cDNA library of human osteosarcoma cell line Saos-2 revealed the structure consisting of a 42-bp 5'-untranslated region, a 588-bp ORF, and a 750-bp 3'-untranslated region. Although the 49th amino acid residue is encoded by a stop codon, it is likely that this codon encodes selenocysteine from the molecular weight

of the translation product and the sequence comparison data with the *Caenorhabditis elegans* homologue. The ORF codes for a protein consisting of 195 amino acid residues and there existed a putative secretory signal at the N-terminus and one putative transmembrane domain in the intermediate region. Figure 33 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 58 kDa. In this case, the addition of a microsome led to the formation of a product of 56 kDa from which the secretory signal is considered to have been cleaved. Since both of these products are larger than the molecular weight of 22 kDa predicted from the ORF, it is likely that the protein interacts with another protein.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the *Caenorhabditis elegans* hypothetical protein C35C5.3 (EMBL Accession No. Z78417). Table 22 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the *C. elegans* hypothetical protein C35C5.3 (CE). U at position 49 in the amino acid sequence of the protein of the present invention represents selenocysteine. Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 37.9% in the entire region other than the N-terminal region. Cystein was found in the sequence of the *C. elegans* protein at the position corresponding to position 49 encoded by the stop codon (selenocysteine) of the protein of the present invention.

Table 22

HP MRLLLL

5 CE MRIHDELQKQDMSRFGVFIIGVLFFMSVCDVLRTEESHSHDENHVHEKDDEFEAEGDETDS
HP LLVAASAMVRSEASANLGGVPSKRLKMQYATGPLLKFCICVSUGYRRVFEEYMRVISORY
* *.. *** **...*... ..*

CE QSFSQGTEEDHIEVREQSSFVKPTAVHHAKDLPTLRIFYCVSCGYKQAFDQFTTFKEKY
HP PDIRIEGENYLPQPIYRHIAFLSVFKLVLIIGLIIVGKDPFAFFGMQAPSIWQWGQENKV
10 *.....*. * ..* ** *.... *.. *.***. **. * * *
CE PNMPIEGANFAPVLWKAYVAQALS FVKMAVLVLVLGGINPFERFGLGYPQILQHAGNKM
HP YACMMVFFLSNMIENQCMSTGA FEITLNDVPVWSKLES GHLP SMOQLVQILDNEMKLNKH
.***.*.*.*..* .*****. *.. ..****.***.***.*...*.*... .
CE SSCMLVFMLGNLVEQSLISTGA FEVYLGNEQIWSKIESGRVSPQE FMQLIDAQLAVLGK
15 HP MDSIPHRS

CE APVNTE SFGEFOOTV

20 Furthermore, the search of the GenBank using the base
sequences of the present cDNA has revealed the registration
of sequences that shared a homology of 90% or more (for
example, Accession No. AA156969) in ESTs, but, since they
are partial sequences, it can not be judged whether or not
25 any of these sequences codes for the same protein as the
protein of the present invention.

<HP02695> (SEQ ID Nos. 94, 104, and 114)

Determination of the whole base sequence of the cDNA
30 insert of clone HP02695 obtained from cDNA library of human
stomach cancer revealed the structure consisting of a 112-bp
5'-untranslated region, a 1020-bp ORF, and a 160-bp 3'-

untranslated region. The ORF codes for a protein consisting of 339 amino acid residues and there existed three putative transmembrane domains. Figure 34 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 38 kDa that was almost identical with the molecular weight of 38,274 kDa predicted from the ORF.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the rat hypertension-induced protein S-2 fragment (PIR Accession No. 539959). Table 23 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the rat hypertension-induced protein S-2 fragment (RN). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 74.3% in the entire region.

Table 23

HP MNWELLWLLVLCALLLLLVQLLRFLRADGDLTLLWAEWQGRPEWELTDMVVWVTGASS

5 HP GIGEELAYQLSKLGVSLVLSARRVHELERVKRRCLENGNLKEKDILVLPLDLTDTGSHEA
 ****.*****.***.***.
 RN VKRRSLENGNLKEKDILVLPLDLADTSSHDI
 HP ATKAVLQEFGRIDILVNNGGMSQRSCLMDTSLDVYRKLIELNYLGTVSLTKCVLPHMIER
 .**... ** .***... ***.***** ****.***

10 RN ATKTVLQEFGRIDILVNNGGVAHASLVENTNMDIFKVLIEVNYLGTVSLTKCFLPHMMER
 HP KQGKIVTVNSILGIISVPLSIGYCASKHALRGFFNGLRTELATYPGIIVSNICPGPVQSN
 .*****...*
 RN NQGKIVVMKS

15

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. T84331) in ESTs, but, since they are

20 partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

<HP10031> (SEQ ID Nos. 95, 105, and 115)

25

Determination of the whole base sequence of the cDNA insert of clone HP10031 obtained from cDNA library of human osteosarcoma cell line Saos-2 revealed the structure consisting of a 55-bp 5'-untranslated region, a 1464-bp ORF, and a 649-bp 3'-untranslated region. The ORF codes for a

30 protein consisting of 487 amino acid residues and there existed eleven putative transmembrane domains. Figure 35 depicts the hydrophobicity/hydrophilicity profile, obtained

by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of high molecular weight. When expressed in COS7 cells, an expression product of about 55 kDa was observed in the membrane fraction.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the *Caenorhabditis elegans* hypothetical protein CELK07H8 (GenBank Accession No. AF047659). Table 24 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the *C. elegans* hypothetical protein CELK07H8 (CE). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 44.2% in the entire region.

Table 24

HP	MDGTETRQRRLDSCGKPGELGLPHPLSTGGLPVAS
5	CE MKGGGGIGDGKKDYQSAVHEGLTTFDQLGIALEDVGKSMDAETATPGGSLFSRVIFRFRN HP EDGALRAPESQSVTPKPLETEPSRETAWSIGLQVTPPFMFAGLGLSWAGMLLDYFQHPV *...*... . . . *... . ** ** *****.*.. **
10	CE ENSSLKSRTYDHSNDLVNMSVIPAESSVYLFQVLPFAVAGLGMVFAGLVLSIVVTWPL HP FVEVKDLLTLVPPVLVGLKGNLEMTLASRLSTAANTGQIDDPQEQHRVISSNLALIQQVAT * * . . . *...*...***** ** *...*...*.. *****.*****
15	CE FEEIPEILILVPALLGLKGNLEMTLASRLSTLANLGHMDSSKQRKDVVIANLALVQVQAT HP VVGLLAAVAALLLGVSREEVDVAKVELLCASSVLTAFLAALFALGVLMVCIVIGARKLGV **...*... * * * * . . *...*... ** *...*...*...*...*...*...
20	CE VVAFLASAFAAALAFIPSGDFDWAHGALMCASSLATAACSASLVLSLLMVVVIVTSRKYNI HP NPDNIATPIAASLGLDITLSILALVSSFFYR-HKDSRYLTPLVCLSFALTPVWVLIQKQ ****.*****.***.***. . * * . *...*... . * . * * * . ***.
25	CE NPDNVATPIAASLGLDITLTVLAFFGSVFLKAHNTESWLNVIVIVLFLLLLFPFWIKIANE HP SPPIVKILKFGWFPIILAMVISSFGGLILSKTVSKQYKGMIAFTPVICGVGGNLVAIQT . . . * * * *...*...*...*...*...*...*...*...*...*...*...*...*...*...
30	CE NEGTOETLYNGWTPVIMSMLISSAGGFILETAV--RRYHSLSTYGPVLNGVGGNLAAVQA HP SRISTYLHMWSAPGVLPLO--MKKFWPNPCSTFCTSEINSMASRVLLLLLVPGHLIF-FY **...*... . . **** . . . * . . . * . *...*...*...*...*...*...
35	CE SRLSTYFHKAGTVGVLPNEWTVSFR--TSVQRAFFSKEWDSRSARVLLLLLVPGHICFNFL HP I-IYLVGQSVINSQ--TFVVLYLLAGLIQVTILLYLAEVMVRLTWHQALDPDNHCIPYL * * . ***.***.***.***. . . . * * * . ***** ****
40	CE IQLFTLTSKNNVTPHGPLFTSLYMIAAIIQVVILLFVCQLLVALLWKWKIDPDNSVIPYL HP TGLGDLGTLGTLALCFFTDWLLKSKAELGGISELASGPP *...*****. . *..*
45	CE TALGDLGTLGTLFIVFLTTDHFDPKELTSS

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for

example, Accession No. AA334000) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

5

<HP10530> (SEQ ID Nos. 96, 106, and 116)

Determination of the whole base sequence of the cDNA insert of clone HP10530 obtained from cDNA library of human osteosarcoma cell line Saos-2 revealed the structure consisting of a 80-bp 5'-untranslated region, a 1182-bp ORF, and a 95-bp 3'-untranslated region. The ORF codes for a protein consisting of 393 amino acid residues and there existed a putative secretory signal at the N-terminus. Figure 36 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 46 kDa that was somewhat larger than the molecular weight of 44,912 predicted from the ORF. In this case, the addition of a microsome led to the formation of a product of 45.5 kDa from which the secretory signal is considered to have been cleaved. Application of the (-3,-1) rule, a method for predicting the cleavage site of the secretory signal sequence, allows to expect that the mature protein starts from lysine at position 23. When expressed in COS7 cells, an expression product of about 43 kDa was observed in the supernatant fraction and the membrane fraction.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the Arabidopsis thaliana hypothetical protein IG002N01 (GenBank Accession No. AF007269). Table 25 shows the comparison between amino acid sequences of the

30

human protein of the present invention (HP) and the A.
thaliana hypothetical protein IG002N01 (AT). Therein, the
marks of -, *, and . represent a gap, an amino acid residue
identical with that of the protein of the present invention,
5 and an amino acid residue similar to that of the protein of
the present invention, respectively. The both proteins
shared a homology of 27.0% in the N-terminal region of 355
amino acid residues.

Table 25

[illegible]

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA302913) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the

protein of the present invention.

<HP10541> (SEQ ID Nos. 97, 107, and 117)

Determination of the whole base sequence of the cDNA
5 insert of clone HP10541 obtained from cDNA library of human
stomach cancer revealed the structure consisting of a 7-bp
5'-untranslated region, a 591-bp ORF, and a 113-bp 3'-
untranslated region. The ORF codes for a protein consisting
of 196 amino acid residues and there existed a putative
10 secretory signal at the N-terminus. Figure 37 depicts the
hydrophobicity/hydrophilicity profile, obtained by the Kyte-
Doolittle method, of the present protein. In vitro
translation resulted in formation of a translation product
of 23 kDa that was somewhat larger than the molecular weight
15 of 21,553 predicted from the ORF. In this case, the addition
of a microsome led to the formation of a product of 20 kDa
from which the secretory signal is considered to have been
cleaved and a product of 23 kDa which is considered to have
a sugar chain being attached. Application of the (-3,-1)
20 rule, a method for predicting the cleavage site of the
secretory signal sequence, allows to expect that the mature
protein starts from glycine at position 41. In addition,
there exists in the amino acid sequence of this protein one
site at which N-glycosylation may occur (Asn-Leu-Thr at
25 position 185).

The search of the protein data base using the amino
acid sequence of the present protein revealed that the
protein was similar to the human zymogen membrane protein
(GenBank Accession No. AF056492). Table 26 shows the
30 comparison between amino acid sequences of the human protein
of the present invention (HP) and the human zymogen membrane
protein (ZM). Therein, the marks of -, *, and . represent a

gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 37.6% in the C-terminal region of 133 amino acid residues.

Table 26

10	HP MWRVPGTTRRPVTGESPGMHRPEAMLLLLTLALLGGPTWAGKMYGPGGGKYFS--TTEDYD	**.***** ** *
	ZM MLTVALLALLCASASGNAIQARSSSYSGEYGSGGGKRFSHSGNQLD	
	HP HEITGLRVSVGLLLVKSVQVKLGDSWDVKLGALGGNTQEVTLQPGEYITKVVFVAFQAFRLR	
		.**.*. . .****. *. *. .*. .*. .*. *.******.
	ZM GPITALRVRVNTYYIVGLQVRYGKVWSDYVGGRNGLDLEEIFLHPGESVIQVSGKYKWYLK	
15	HP GMVMYTSKDRYFYFGKLDGQISSAYPSQEGQVLVGIYGQYQLLGIKSIGFEWN-YPLEEP	
		.*. *.****. *** .* .* * . . ** * *. * *.....**
	ZM KLVFVTDKGRYLSFGKDSGTSFNAVPLHPNTVLRFISGRSGSL-IDAIGLHWDVYPTSCS	
	HP TTEPPVNLTYSANSPVGR	
20	ZM RC	

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA340605) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

<HP10550> (SEQ ID Nos. 98, 108, and 118)

Determination of the whole base sequence of the cDNA

insert of clone HP10550 obtained from cDNA library of human stomach cancer revealed the structure consisting of a 241-bp 5'-untranslated region, a 324-bp ORF, and a 86-bp 3'-untranslated region. The ORF codes for a protein consisting of 107 amino acid residues and there existed one putative transmembrane domain. Figure 38 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of high molecular weight.

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA348310) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

<HP10590> (SEQ ID Nos. 99, 109, and 119)

Determination of the whole base sequence of the cDNA insert of clone HP10590 obtained from cDNA library of human fibrosarcoma cell line HT-1080 revealed the structure consisting of a 77-bp 5'-untranslated region, a 1053-bp ORF, and a 180-bp 3'-untranslated region. The ORF codes for a protein consisting of 350 amino acid residues and there existed one putative transmembrane domain. Figure 39 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 40 kDa that was almost identical with the molecular weight of 39,285 predicted from the ORF. In this case, the addition of a microsome led to the formation of a product of

43 kDa which is considered to have a sugar chain being attached. In addition, there exist in the amino acid sequence of this protein two sites at which N-glycosylation may occur (Asn-Asn-Ser at position 144 and Asn-Leu-Thr at position 328).

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA461346) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

<HP10591> (SEQ ID Nos. 100, 110, and 120)

Determination of the whole base sequence of the cDNA insert of clone HP10591 obtained from cDNA library of human fibrosarcoma cell line HT-1080 revealed the structure consisting of a 232-bp 5'-untranslated region, a 324-bp ORF, and a 844-bp 3'-untranslated region. The ORF codes for a protein consisting of 107 amino acid residues and there existed one putative transmembrane domain. Figure 40 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 12 kDa that was almost identical with the molecular weight of 11,328 predicted from the ORF.

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. H09424) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein

of the present invention.

<HP01462> (SEQ ID Nos. 121, 131, and 141)

Determination of the whole base sequence of the cDNA
5 insert of clone HP01462 obtained from cDNA library of human
fibrosarcoma cell line HT-1080 revealed the structure
consisting of a 121-bp 5'-untranslated region, a 1452-bp ORF,
and a 477-bp 3'-untranslated region. The ORF codes for a
protein consisting of 483 amino acid residues and there
10 existed a putative secretory signal at the N-terminus.
Figure 41 depicts the hydrophobicity/hydrophilicity profile,
obtained by the Kyte-Doolittle method, of the present
protein. In vitro translation resulted in formation of a
translation product of 72 kDa that was larger than the
15 molecular weight of 55,838 predicted from the ORF.
Application of the (-3,-1) rule, a method for predicting the
cleavage site of the secretory signal sequence, allows to
expect that the mature protein starts from lysine at
position 21.

20 The search of the protein data base using the amino
acid sequence of the present protein revealed that the
protein was similar to the *Caenorhabditis elegans*
hypothetical protein ZK1058.4 (EMBL Accession No. Z35604).
Table 27 shows the comparison between amino acid sequences
25 of the human protein of the present invention (HP) and the *C.*
elegans hypothetical protein ZK1058.4 (CE). Therein, the
marks of -, *, and . represent a gap, an amino acid residue
identical with that of the protein of the present invention,
and an amino acid residue similar to that of the protein of
30 the present invention, respectively. The both proteins
shared a homology of 35.6% in the entire region.

Table 27

HP MKAFHTFCVVLLVFGSVSEAKFDDFEDEEDIVEYDDNDFAEFEDVMEDSVTESPQRVIIT
☆ ☆

5 CE MKIVWIFLIFFIGFAIST
HP EDDE-DETTVELEGQDENQEGDFEDADTQEGDTESEPYDDEEFEGYEDKP-----D
*. * . * . * . . . * * . * . . . *
CE DDNEFAEFEDFVGSSATQAPEIQREGEPPVLKQKDDFEEDFGVVEEPEEAEKVREAD
HP TSSSKNKDPITIVDVPAPHLQNSWESYYLEILMVTGLLAYIMNYIIGKNKNSRLAQAWFNT
10 * * * . * . * . * * .
CE SDDAAPAQPLKFADVPAHFRSNWASYQVEGIVVLIILYIMTNYLIGKTTNASIAQTIFDM
HP HRELLESNFTLVGDDGTNKEATSTGKLNQENEHIYNLWCSGRVCCEGMLIQLRFLKRQDL
* * * * * * * .
CE CRPTLEEQFAVVGDDGTTDLDKMIPSLKHDTSTFSAWCTGRVNVNSLFLQMKMVKRQDV
15 HP LNVLARMMPVSDQVQIKVTMN-DEDMDTYVFAVGTRKALVRLQEMQDLSEFCSDKPKS
.. . * . * . * * . * . . * * *
CE VSRIMEMFTPSGDKMTIKASLETTNDTDPLIFAVGEKKIASKYFKEMLDLNSFASERKQA
HP GAKYGLPDSLAILSEMGEVTDGMMDTKMVHFLTHYADKIESVHFSDQFSGPKIMQEEGQP
..... * . * . . . * * . * . . . * * *
20 CE AQQFNLPASWQVYADQNEVVSILDPGVVSLKKHEDAIEFIHISDQFTGPKPAEGESYT
HP LKLPDTKRTLFTFNVPGSGNTYPKDMEALLPLNMNVIYSIDKAKKFRNLNREGKQKADKN
* * * * * * *
CE -RLPEAQRYMFVSLNLQYLG---QDEESVMEILNLVLYLIDKARKMKLSKDAKVAERR
HP RARVEENFLKLTHVQRQEAASRREEKKRAEKERIMNEEDPEKQRRLEEAALRREQKKLE
25 * * * * * * * *
CE RKEFEDAFLLKQTHQFRQEAQAARREEKTRERKQKLMDSDPERQKRLEAKELKREKA--
HP KKQMKMKQIKVKAM
* * * * * * *
CE -KSPKMKQLKVK

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for

example, Accession No. AA307793) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

5

<HP02485> (SEQ ID Nos. 122, 132, and 142)

Determination of the whole base sequence of the cDNA insert of clone HP02485 obtained from cDNA library of human stomach cancer revealed the structure consisting of a 69-bp
10 5'-untranslated region, a 1005-bp ORF, and a 1672-bp 3'-untranslated region. The ORF codes for a protein consisting of 334 amino acid residues and there existed one putative transmembrane domain. Figure 42 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-
15 Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 36 kDa that was almost identical with the molecular weight of 38,171 predicted from the ORF. When expressed in COS7 cells, an expression product of about 23 kDa was
20 observed in the membrane fraction.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the *Caenorhabditis elegans* hypothetical protein W01A11.2 (GenBank Accession No. U64852).
25 Table 28 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the *C. elegans* hypothetical protein W01A11.2 (CE). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of
30 the present invention, respectively. The both proteins shared a homology of 45.5% in the entire region.

[illegible]

Furthermore, the search of the GenBank using the base
sequences of the present cDNA has revealed the registration
of sequences that shared a homology of 90% or more (for
example, Accession No. D25664) in ESTs, but, since they are
partial sequences, it can not be judged whether or not any
of these sequences codes for the same protein as the protein
of the present invention.

<HP02798> (SEQ ID Nos. 123, 133, and 143)

Determination of the whole base sequence of the cDNA

insert of clone HP02798 obtained from cDNA library of human fibrosarcoma cell line HT-1080 revealed the structure consisting of a 31-bp 5'-untranslated region, a 804-bp ORF, and a 301-bp 3'-untranslated region. The ORF codes for a protein consisting of 267 amino acid residues and there existed four putative transmembrane domains. Figure 43 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 29 kDa that was almost identical with the molecular weight of 30,778 predicted from the ORF. When expressed in COS7 cells, an expression product of about 26 kDa was observed in the membrane fraction.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the human DHHC-containing cysteine-rich protein (GenBank Accession No. U90653). Table 29 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the human DHHC-containing cysteine-rich protein (DH). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 35.0% in the intermediate region of 100 amino acid residues. The positions of seven cysteines were conserved between the two proteins. The protein of the present invention also had the DHHC (Asp-His-His-Cys) sequence.

Table 29

HP MAPWALLSPGVLVRTGHTVLTWGI

5 DH MYKMNICNKPSNKTAPESVWTAPAQPSGPSPELQGQRRNRNGWSWPPHPLQIVAWLLYL
HP TLVFLHDTLRLQWEEQGELLPLTFLLLVLGSLLLYLAVSLMDPGYVNVQPQP-QEELK
* * * . * . . . *
DH FFAVIGFGILVPLLPHHWVPAGYACMGAIFAGHLVVHLTAVSIDPADDNVRDKSYAGPLP
HP EEQTAMVPPAIPLRRCRYCLVLQPLRARHCRECRRCVRRYDHHCPWMENCVGERNHPLFV
10 * . * . * . * * . * . . . * . * . . . * . * . . . *
DH IFNRSQHAHVIEDLHCNLCNVDVSARSKHCSACNKCVCGFDDHCKWLNNCVGERNYRFLF
HP VYLALQLVLVLLWGLYLAWSGLRFFQPWGLWLRSSGLLFATFLLLSLFSLVASLLLVSHTLY
. * . * . *
DH HSVASALLGVLLLVLGGHICLRGVLCQPHASAHQPTL

15

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. D79050) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

<HP10041> (SEQ ID Nos. 124, 134, and 144)

Determination of the whole base sequence of the cDNA insert of clone HP10041 obtained from cDNA library of human osteosarcoma cell line Saos-2 revealed the structure consisting of a 12-bp 5'-untranslated region, a 321-bp ORF, and a 286-bp 3'-untranslated region. The ORF codes for a protein consisting of 106 amino acid residues and there existed one putative transmembrane domain. Figure 44 depicts

the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 12 kDa that was almost identical with the molecular weight of 12,060 predicted from the ORF. When expressed in COS7 cells, an expression product of about 13 kDa was observed in the membrane fraction.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the *Caenorhabditis elegans* hypothetical protein K10B2.4 (GenBank Accession No. U28730). Table 30 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the *C. elegans* hypothetical protein K10B2.4 (CE). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The both proteins shared a homology of 62.1% in the entire region.

Table 30

HP	MSTNNMSDPRRPNKVLRYKP---PPSECNPALDDPTPDYMNLLGMIFSMCGLMLKLKWCA
	.****.*...****** *.****.*****.....****.
CE	MQQNGDPRRTNRIVRYKPLDSTANQQQAISEDPLPEYMNVLGMIFSMCGLMIRMKWCS
HP	WVAVYCSFISFANSRSEDTKQMMSSFMLSISAVVMSYLQNPQPMTPPW
	.. ** *****.*.*.*.....*****.***** *..***
CE	WLALVCSCISFANTRTSDDAKQIVSSFMLSVSAVVMSYLQNPSPPIPPWVTLTLLQS

Furthermore, the search of the GenBank using the base

sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. H20098) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

<HP10246> (SEQ ID Nos. 125, 135, and 145)

Determination of the whole base sequence of the cDNA insert of clone HP10246 obtained from cDNA library of human epidermoid carcinoma cell line KB revealed the structure consisting of a 110-bp 5'-untranslated region, a 675-bp ORF, and a 79-bp 3'-untranslated region. The ORF codes for a protein consisting of 224 amino acid residues and there existed five putative transmembrane domains. Figure 45 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 23 kDa that was somewhat smaller than the molecular weight of 25,244 predicted from the ORF. When expressed in COS7 cells, an expression product of about 21 kDa was observed in the membrane fraction.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the human putative seven transmembrane domain protein (GenBank Accession No. Y18007). Table 31 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the human putative seven transmembrane domain protein (TM). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that

of the protein of the present invention, respectively. The both proteins shared a homology of 93.3% in the entire region.

5

Table 31

```

HP MTLFHFGNCFALAYFPYFITYKCSGLSEYNAFWKCVQAGVTYLFVQLCKMLFLATFFPTW
*****.*****
TM MTLFHFGNCFALAYFPYFITYKCTDLSEYNAFWKCVQAGVTYLFVQLCKMLFLATFFPTW
10 HP EGGIYDFIGEFMKASVDVADLIGLNLVMSRNAGKGEYKIMVAALGWATAELIMSRCIPLW
*****
TM EGGIYDFIGEFMKASVDVADLIGLNLVMSRNAGKGEYKIMVAALGWATAELIMSRCIPLW
HP VGARGIEFDWKYIQMSIDSNISLVHYIVASAQVWMITRYDLYHTFRPAVLLLMFLSVYKA
*****.*****
15 TM VGARGIEFDWKYIQMSIDSNISLGPYIVASAQVWMITRYDLYHTFRPAVLLLMFLRVYKA
HP FVMETFVHLCSLGSLGWAALLARAVVTGLLALSTLALYVAVVNVHS
*****.*.*.***.***.....*.*****
TM FVMETFVHLCSLGSLGSAVLMAGVVVKGLLVIRNLAMYVAVVNVHS

```

20

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA453931) in ESTs, but, since they

25 are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

30

<HP10392> (SEQ ID Nos. 126, 136, and 146)

Determination of the whole base sequence of the cDNA insert of clone HP10392 obtained from cDNA library of human osteosarcoma cell line U-2 OS revealed the structure

consisting of a 24-bp 5'-untranslated region, a 777-bp ORF, and a 726-bp 3'-untranslated region. The ORF codes for a protein consisting of 258 amino acid residues and there existed a putative secretory signal at the N-terminus.

5 Figure 46 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 34 kDa that was somewhat larger than the molecular weight of 29,623 predicted from the ORF.
10 Application of the (-3,-1) rule, a method for predicting the cleavage site of the secretory signal sequence, allows to expect that the mature protein starts from leucine at position 49.

Furthermore, the search of the GenBank using the base
15 sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. H15999) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein
20 of the present invention. In addition, partial identity with the hypothetical protein KIAA0384 (Accession No. AB002382) was observed, although the hypothetical protein had a different ORF.

25 <HP10489> (SEQ ID Nos. 127, 137, and 147)

Determination of the whole base sequence of the cDNA insert of clone HP10489 obtained from cDNA library of human stomach cancer revealed the structure consisting of a 137-bp 5'-untranslated region, a 333-bp ORF, and a 189-bp 3'-
30 untranslated region. The ORF codes for a protein consisting of 110 amino acid residues and there existed two putative transmembrane domains. Figure 47 depicts the

hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 19 kDa that was somewhat larger than the molecular weight of 12,010 predicted from the ORF.

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. AA262162) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein of the present invention.

<HP10519> (SEQ ID Nos. 128, 138, and 148)

Determination of the whole base sequence of the cDNA insert of clone HP10519 obtained from cDNA library of human stomach cancer revealed the structure consisting of a 67-bp 5'-untranslated region, a 276-bp ORF, and a 367-bp 3'-untranslated region. The ORF codes for a protein consisting of 91 amino acid residues and there existed one putative transmembrane domain. Figure 48 depicts the hydrophobicity/hydrophilicity profile, obtained by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of 10 kDa that was almost identical with the molecular weight of 10,275 predicted from the ORF.

Furthermore, the search of the GenBank using the base sequences of the present cDNA has revealed the registration of sequences that shared a homology of 90% or more (for example, Accession No. W16639) in ESTs, but, since they are partial sequences, it can not be judged whether or not any of these sequences codes for the same protein as the protein

of the present invention.

<HP10531> (SEQ ID Nos. 129, 139, and 149)

Determination of the whole base sequence of the cDNA
5 insert of clone HP10531 obtained from cDNA library of human
osteosarcoma cell line Saos-2 revealed the structure
consisting of a 55-bp 5'-untranslated region, a 1035-bp ORF,
and a 1092-bp 3'-untranslated region. The ORF codes for a
protein consisting of 344 amino acid residues and there
10 existed five putative transmembrane domains. Figure 49
depicts the hydrophobicity/hydrophilicity profile, obtained
by the Kyte-Doolittle method, of the present protein. In
vitro translation resulted in formation of a translation
product of high molecular weight.

15 Furthermore, the search of the GenBank using the base
sequences of the present cDNA has revealed the registration
of sequences that shared a homology of 90% or more (for
example, Accession No. R50695) in ESTs, but, since they are
partial sequences, it can not be judged whether or not any
20 of these sequences codes for the same protein as the protein
of the present invention.

<HP10574> (SEQ ID Nos. 130, 140, and 150)

Determination of the whole base sequence of the cDNA
25 insert of clone HP10574 obtained from cDNA library of human
stomach cancer revealed the structure consisting of a 210-bp
5'-untranslated region, a 1287-bp ORF, and a 1276-bp 3'-
untranslated region. The ORF codes for a protein consisting
of 428 amino acid residues and there existed a putative
30 secretory signal at the N-terminus and one putative
transmembrane domain in the intermediate region. Figure 50
depicts the hydrophobicity/hydrophilicity profile, obtained

by the Kyte-Doolittle method, of the present protein. In vitro translation resulted in formation of a translation product of high molecular weight. Application of the (-3,-1) rule, a method for predicting the cleavage site of the secretory signal sequence, allows to expect that the mature protein starts from serine at position 36.

The search of the protein data base using the amino acid sequence of the present protein revealed that the protein was similar to the *Drosophila melanogaster* GOLIATH protein (SWISS-PROT Accession No. Q06003). Table 32 shows the comparison between amino acid sequences of the human protein of the present invention (HP) and the *D. melanogaster* GOLIATH protein (DM). Therein, the marks of -, *, and . represent a gap, an amino acid residue identical with that of the protein of the present invention, and an amino acid residue similar to that of the protein of the present invention, respectively. The intermediate region of 169 amino acids of the protein of the present invention shared a homology of 41.4% with the N-terminal region of the *D. melanogaster* GOLIATH protein.

Table 32

HP MGPPPGAGVSCRGGCGFSRLLAWCFLLALS PQAPGSRGAEAVWTAYLNVSWRVPHTGVNR
HP TVWELSEEGVYGQDSPLEPVAGVLVPPDGP GALNACNPHNTFTVPTVWGSTVQVSWLALI
5 HP QRGGGCTFADKIH LAYERGASGAVIFNFPGTRNEVIPMSHPGAVDIVAIMIGNLKGTKIL
DM M QLEKMQIKGKTRNIAAVITYQNIQDLS
HP QSIQRGIQVTMVIEWGKK--HGPWVNHYISIFFVSVSFFIITAATVGYFIFYSARRLRNA
DM LTLDKGYNVTISIIEGRRGVRTISSLNRTSVL FVSIS-FIV-DDILCWLIFYIYIQRFRYM
0 HP RAQSRKQ RQLKADAKKAIGRLQLRTLKQGDKEIGPDGDS CAVCIELYKPNDLVRILT CNH
DM QAKDQQSRNLCSVT KKAIMKIPTKTGKFSD-EKDLDS DCCAICIEAYKPTDTIRILPCKH
HP IFHKTCVDPWLLEHRTCPMCKCDILKALGIEVDVEDGSVSLQVPVSNEISNSASSHEEDN
5 DM EFHKNCIDPWLIEHRTCPMCKLDVLKFYGYVVG DQIYQTPSPQHTAPIASIEEVPVIVVA
HP RSETASSGYASVQGTDEPPLEEHVQSTNESLQLVNHEANSVAVDVIPHDNPTFEEDETP
DM VPHGPQPLQPLQASNMSSFAPSHYFQSSRSPSSSVQQQLAPLTYQPHPQQAASERGRNS
0 HP NQETAVREIKS
DM APATMPHAITASHQVTDV

25 Furthermore, the search of the GenBank using the base
sequences of the present cDNA has revealed the registration
of sequences that shared a homology of 90% or more (for
example, Accession No. AA155685) in ESTs, but, since they
are partial sequences, it can not be judged whether or not
30 any of these sequences codes for the same protein as the
protein of the present invention.

INDUSTRIAL APPLICABILITY

The present invention provides human proteins having hydrophobic domains, DNAs coding for these proteins, and expression vectors for these DNAs as well as eucaryotic cells expressing these DNAs. All of the proteins of the present invention are secreted or exist in the cell membrane, so that they are considered to be proteins controlling the proliferation and/or the differentiation of the cells. Accordingly, the proteins of the present invention can be employed as pharmaceuticals such as carcinostatic agents which act to control the proliferation and/or the differentiation of the cells, or as antigens for preparing antibodies against these proteins. The DNAs of the present invention can be utilized as probes for the genetic diagnosis and gene sources for the gene therapy. Furthermore, the DNAs can be utilized for large-scale expression of these proteins. Cells into which these genes are introduced to express these proteins, can be utilized for detection of the corresponding receptors and ligands, screening of novel low-molecular pharmaceuticals, and so on.

The present invention also provides genes corresponding to the polynucleotide sequences disclosed herein. "Corresponding genes" are the regions of the genome that are transcribed to produce the mRNAs from which cDNA polynucleotide sequences are derived and may include contiguous regions of the genome necessary for the regulated expression of such genes. Corresponding genes may therefore include but are not limited to coding sequences, 5' and 3' untranslated regions, alternatively spliced exons, introns, promoters, enhancers, and silencer or suppressor elements. The corresponding genes can be isolated in accordance with known methods using the sequence information disclosed herein. Such methods include the preparation of probes or

primers from the disclosed sequence information for identification and/or amplification of genes in appropriate genomic libraries or other sources of genomic materials. An "isolated gene" is a gene that has been separated from the adjacent coding sequences, if any, present in the genome of the organism from which the gene was isolated.

Organisms that have enhanced, reduced, or modified expression of the gene(s) corresponding to the polynucleotide sequences disclosed herein are provided. The desired change in gene expression can be achieved through the use of antisense polynucleotides or ribozymes that bind and/or cleave the mRNA transcribed from the gene (Albert and Morris, 1994, Trends Pharmacol. Sci. 15(7): 250-254; Lavarosky et al., 1997, Biochem. Mol. Med. 62(1): 11-22; and Hampel, 1998, Prog. Nucleic Acid Res. Mol. Biol. 58: 1-39; all of which are incorporated by reference herein). Transgenic animals that have multiple copies of the gene(s) corresponding to the polynucleotide sequences disclosed herein, preferably produced by transformation of cells with genetic constructs that are stably maintained within the transformed cells and their progeny, are provided. Transgenic animals that have modified genetic control regions that increase or reduce gene expression levels, or that change temporal or spatial patterns of gene expression, are also provided (see European Patent No. 0 649 464 B1, incorporated by reference herein). In addition, organisms are provided in which the gene(s) corresponding to the polynucleotide sequences disclosed herein have been partially or completely inactivated, through insertion of extraneous sequences into the corresponding gene(s) or through deletion of all or part of the corresponding gene(s). Partial or complete gene inactivation can be accomplished

through insertion, preferably followed by imprecise excision, of transposable elements (Plasterk, 1992, Bioessays 14(9): 629-633; Zwaal et al., 1993, Proc. Natl. Acad. Sci. USA 90(16): 7431-7435; Clark et al., 1994, Proc. Natl. Acad. Sci. USA 91(2): 719-722; all of which are incorporated by reference herein), or through homologous recombination, preferably detected by positive/negative genetic selection strategies (Mansour et al., 1988, Nature 336: 348-352; U.S. Patent Nos. 5,464,764; 5,487,992; 5,627,059; 5,631,153; 5,614, 396; 5,616,491; and 5,679,523; all of which are incorporated by reference herein). These organisms with altered gene expression are preferably eukaryotes and more preferably are mammals. Such organisms are useful for the development of non-human models for the study of disorders involving the corresponding gene(s), and for the development of assay systems for the identification of molecules that interact with the protein product(s) of the corresponding gene(s). Where the protein of the present invention is membrane-bound (e.g., is a receptor), the present invention also provides for soluble forms of such protein. In such forms part or all of the intracellular and transmembrane domains of the protein are deleted such that the protein is fully secreted from the cell in which it is expressed. The intracellular and transmembrane domains of proteins of the invention can be identified in accordance with known techniques for determination of such domains from sequence information.

Proteins and protein fragments of the present invention include proteins with amino acid sequence lengths that are at least 25% (more preferably at least 50%, and most preferably at least 75%) of the length of a disclosed protein and have at least 60% sequence identity (more

preferably, at least 75% identity; most preferably at least 90% or 95% identity) with that disclosed protein, where sequence identity is determined by comparing the amino acid sequences of the proteins when aligned so as to maximize overlap and identity while minimizing sequence gaps. Also included in the present invention are proteins and protein fragments that contain a segment preferably comprising 8 or more (more preferably 20 or more, most preferably 30 or more) contiguous amino acids that shares at least 75% sequence identity (more preferably, at least 85% identity; most preferably at least 95% identity) with any such segment of any of the disclosed proteins.

Species homologs of the disclosed polynucleotides and proteins are also provided by the present invention. As used herein, a "species homologue" is a protein or polynucleotide with a different species of origin from that of a given protein or polynucleotide, but with significant sequence similarity to the given protein or polynucleotide, as determined by those of skill in the art. Species homologs may be isolated and identified by making suitable probes or primers from the sequences provided herein and screening a suitable nucleic acid source from the desired species.

The invention also encompasses allelic variants of the disclosed polynucleotides or proteins; that is, naturally-occurring alternative forms of the isolated polynucleotide which also encode proteins which are identical, homologous, or related to that encoded by the polynucleotides.

The invention also includes polynucleotides with sequences complementary to those of the polynucleotides disclosed herein.

The present invention also includes polynucleotides

capable of hybridizing under reduced stringency conditions,
more preferably stringent conditions, and most preferably
highly stringent conditions, to polynucleotides described
herein. Examples of stringency conditions are shown in the
5 table 33 below: highly stringent conditions are those that
are at least as stringent as, for example, conditions A-F;
stringent conditions are at least as stringent as, for
example, conditions G-L; and reduced stringency conditions
are at least as stringent as, for example, conditions M-R.

10

Table 33

Stringency Condition	Polynucleotide Hybrid	Hybrid Length (bp) [‡]	Hybridization Temperature and Buffer [†]	Wash Temperature and Buffer [†]
A	DNA : DNA	≥50	65°C; 1×SSC -or- 42°C; 1×SSC, 50% formamide	65°C; 0.3×SSC
B	DNA : DNA	<50	T _B *; 1×SSC	T _B *; 1×SSC
C	DNA : RNA	≥50	67°C; 1×SSC -or- 45°C; 1×SSC, 50% formamide	67°C; 0.3×SSC
D	DNA : RNA	<50	T _D *; 1×SSC	T _D *; 1×SSC
E	RNA : RNA	≥50	70°C; 1×SSC -or- 50°C; 1×SSC, 50% formamide	70°C; 0.3×SSC
F	RNA : RNA	<50	T _F *; 1×SSC	T _F *; 1×SSC
G	DNA : DNA	≥50	65°C; 4×SSC -or- 42°C; 4×SSC, 50% formamide	65°C; 1×SSC
H	DNA : DNA	<50	T _H *; 4×SSC	T _H *; 4×SSC
I	DNA : RNA	≥50	67°C; 4×SSC -or- 45°C; 4×SSC, 50% formamide	67°C; 1×SSC
J	DNA : RNA	<50	T _J *; 4×SSC	T _J *; 4×SSC
K	RNA : RNA	≥50	70°C; 4×SSC -or- 50°C; 4×SSC, 50% formamide	67°C; 1×SSC
L	RNA : RNA	<50	T _L *; 2×SSC	T _L *; 2×SSC
M	DNA : DNA	≥50	50°C; 4×SSC -or- 40°C; 6×SSC, 50% formamide	50°C; 2×SSC
N	DNA : DNA	<50	T _N *; 6×SSC	T _N *; 6×SSC
O	DNA : RNA	≥50	55°C; 4×SSC -or- 42°C; 6×SSC, 50% formamide	55°C; 2×SSC
P	DNA : RNA	<50	T _P *; 6×SSC	T _P *; 6×SSC
Q	RNA : RNA	≥50	60°C; 4×SSC -or- 45°C; 6×SSC, 50% formamide	60°C; 2×SSC
R	RNA : RNA	<50	T _R *; 4×SSC	T _R *; 4×SSC

‡ : The hybrid length is that anticipated for the hybridized region(s) of the hybridizing polynucleotides. When hybridizing a polynucleotide to a target polynucleotide of unknown sequence, the hybrid length is assumed to be that of the hybridizing polynucleotide. When polynucleotides of known sequence are hybridized, the hybrid length can be determined by aligning the sequences of the polynucleotides and identifying the region or regions of optimal sequence complementarity.

† : SSPE (1×SSPE is 0.15M NaCl, 10mM NaH₂PO₄, and 1.25mM EDTA, pH7.4) can be substituted for SSC (1×SSC is 0.15M NaCl and 15mM sodium citrate) in the hybridization and wash buffers; washes are performed for 15 minutes after hybridization is complete.

*T_B - T_R : The hybridization temperature for hybrids anticipated to be less than

50 base pairs in length should be 5-10°C less than the melting temperature (T_m) of the hybrid, where T_m is determined according to the following equations. For hybrids less than 18 base pairs in length, $T_m(^{\circ}\text{C}) = 2(\text{\# of A + T bases}) + 4(\text{\# of G + C bases})$. For hybrids between 18 and 49 base pairs in length, $T_m(^{\circ}\text{C}) = 81.5 + 16.6(\log_{10}[\text{Na}^+]) + 0.41(\% \text{G+C}) - (600/N)$, where N is the number of bases in the hybrid, and $[\text{Na}^+]$ is the concentration of sodium ions in the hybridization buffer ($[\text{Na}^+]$ for 1×SSC=0.165M).

Additional examples of stringency conditions for polynucleotide hybridization are provided in Sambrook, J., E.F. Fritsch, and T. Maniatis, 1989, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, chapters 9 and 11, and Current Protocols in Molecular Biology, 1995, F.M. Ausubel et al., eds., John Wiley & Sons, Inc., sections 2.10 and 6.3-6.4, incorporated herein by reference.

Preferably, each such hybridizing polynucleotide has a length that is at least 25% (more preferably at least 50%, and most preferably at least 75%) of the length of the polynucleotide of the present invention to which it hybridizes, and has at least 60% sequence identity (more preferably, at least 75% identity; most preferably at least 90% or 95% identity) with the polynucleotide of the present invention to which it hybridizes, where sequence identity is determined by comparing the sequences of the hybridizing polynucleotides when aligned so as to maximize overlap and identity while minimizing sequence gaps.

CLAIMS

1. A protein comprising any one of an amino acid
sequence selected from the group consisting of SEQ ID Nos. 1
5 to 10, 31 to 40, 61 to 70, 91 to 100, and 121 to 130.

2. An isolated DNA coding for the protein according
to Claim 1.

3. An isolated cDNA comprising any one of a base
sequence selected from the group consisting of SEQ ID Nos.
10 11 to 20, 41 to 50, 71 to 80, 101 to 110, and 131 to 140.

4. The cDNA according to Claim 3 consisting of any
one of a base sequence selected from the group consisting of
SEQ ID Nos. 21 to 30, 51 to 60, 81 to 90, 111 to 120, and
141 to 150.

15 5. An expression vector that is capable of expressing
the DNA according to any one of Claim 2 to Claim 4 by in
vitro translation or in eucaryotic cells.

20 6. A transformed eucaryotic cell that is capable of
expressing the DNA according to any one of Claim 2 to Claim
4 and of producing the protein according to Claim 1.

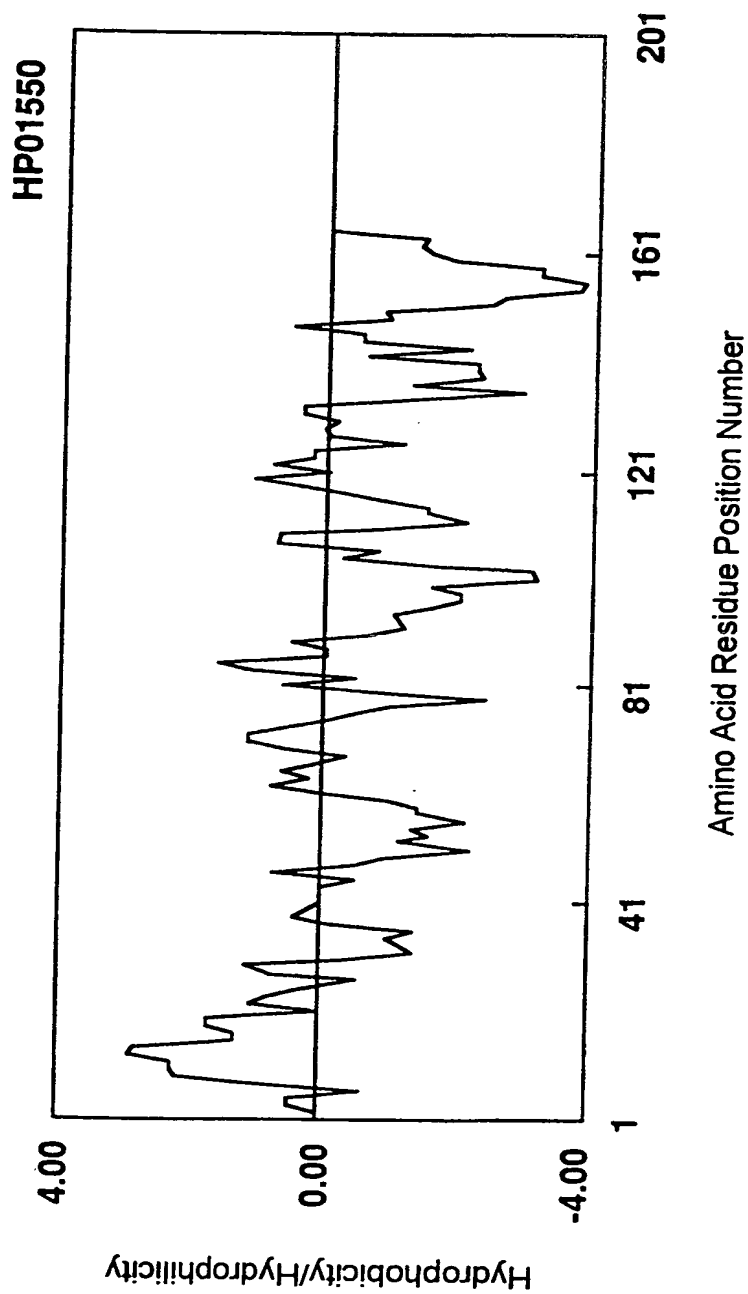


Fig. 1

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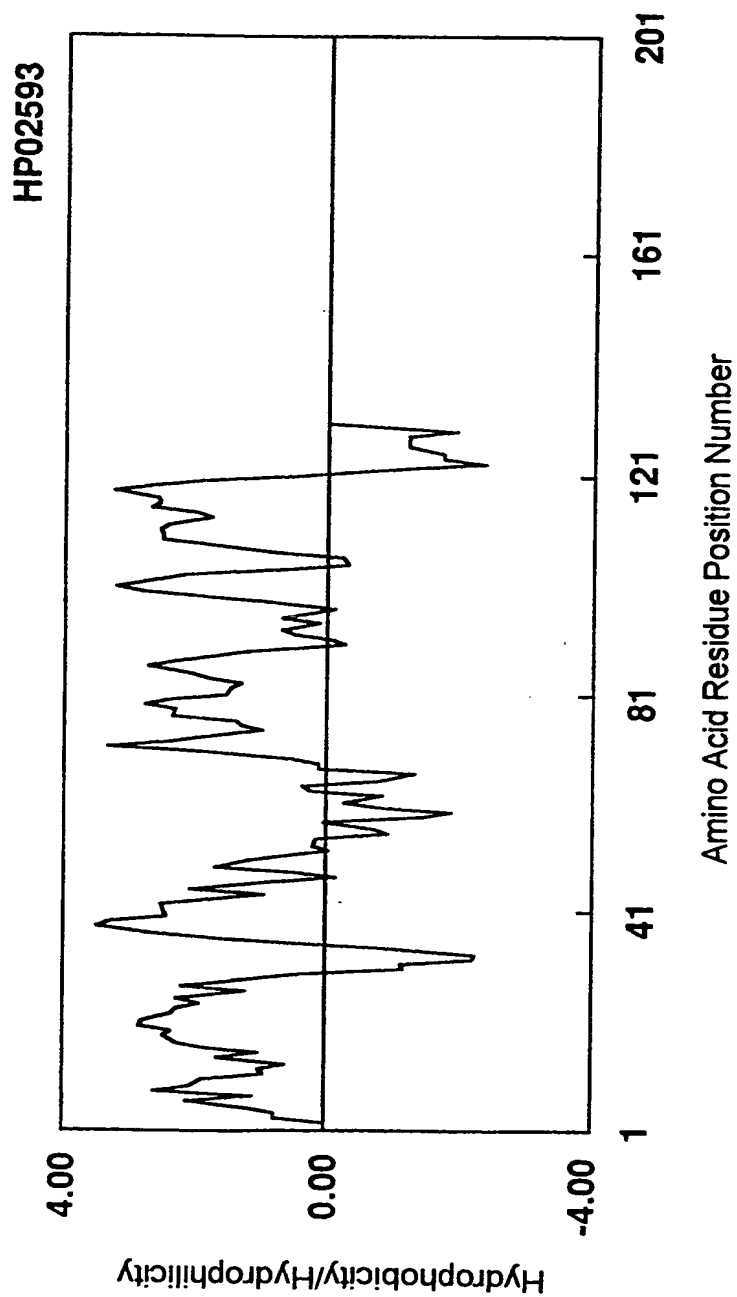


Fig. 2

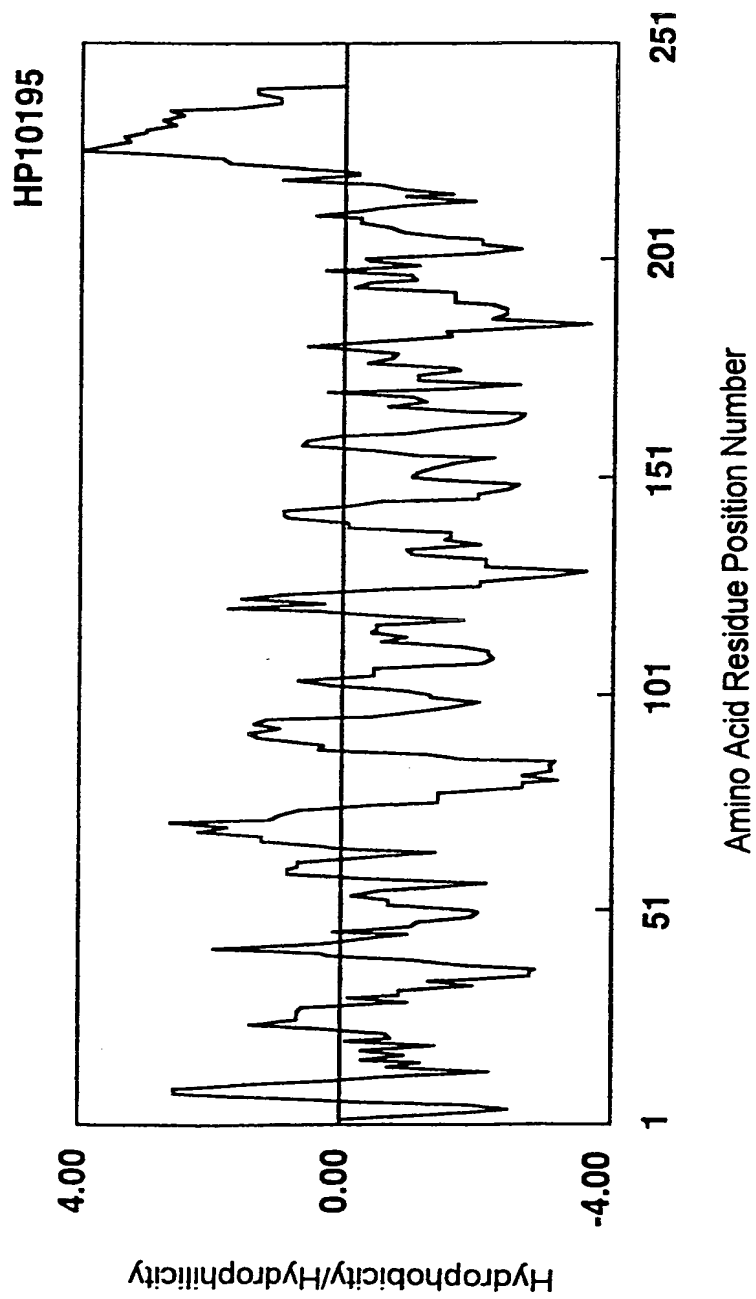


Fig. 3

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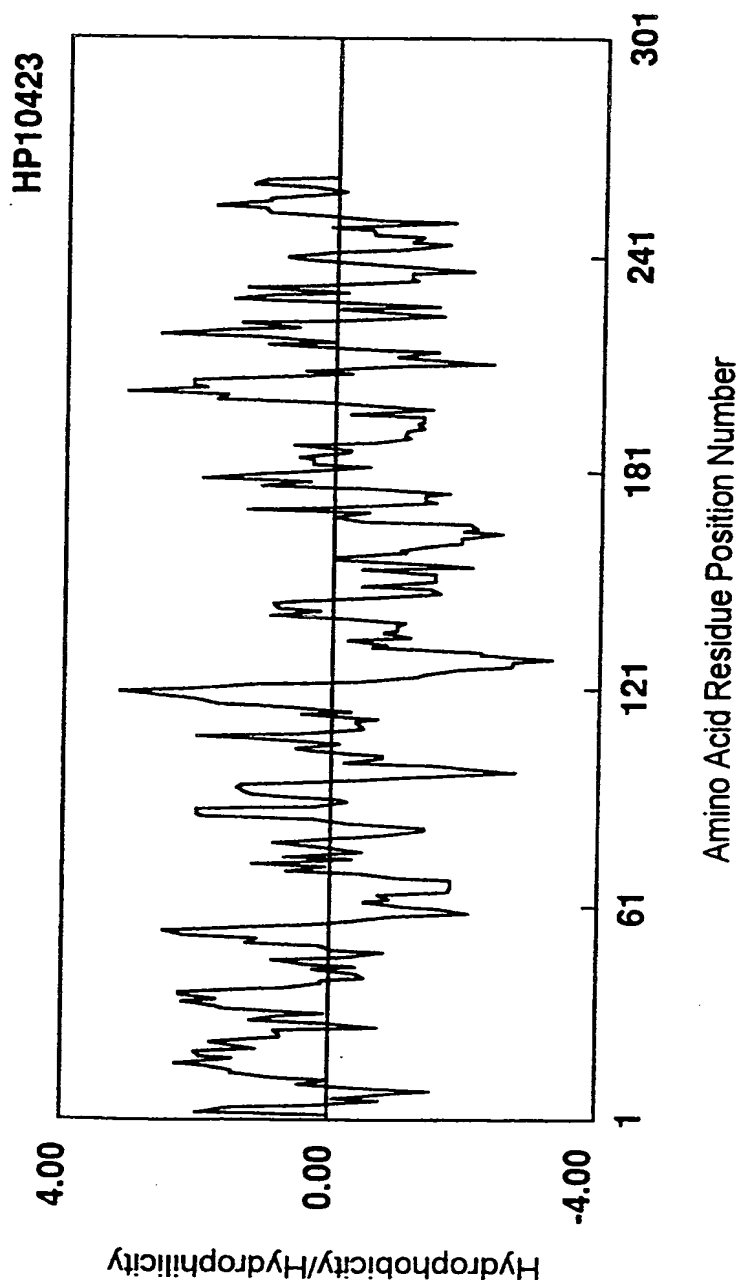


Fig. 4

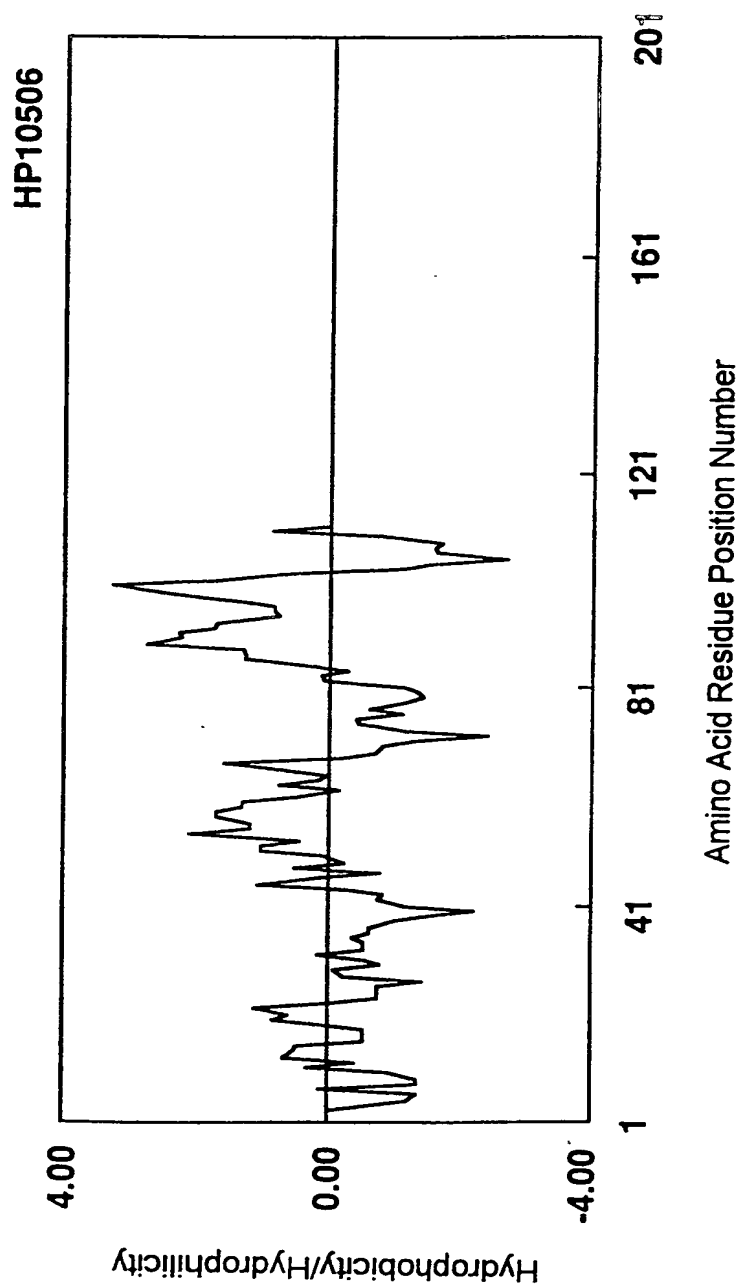


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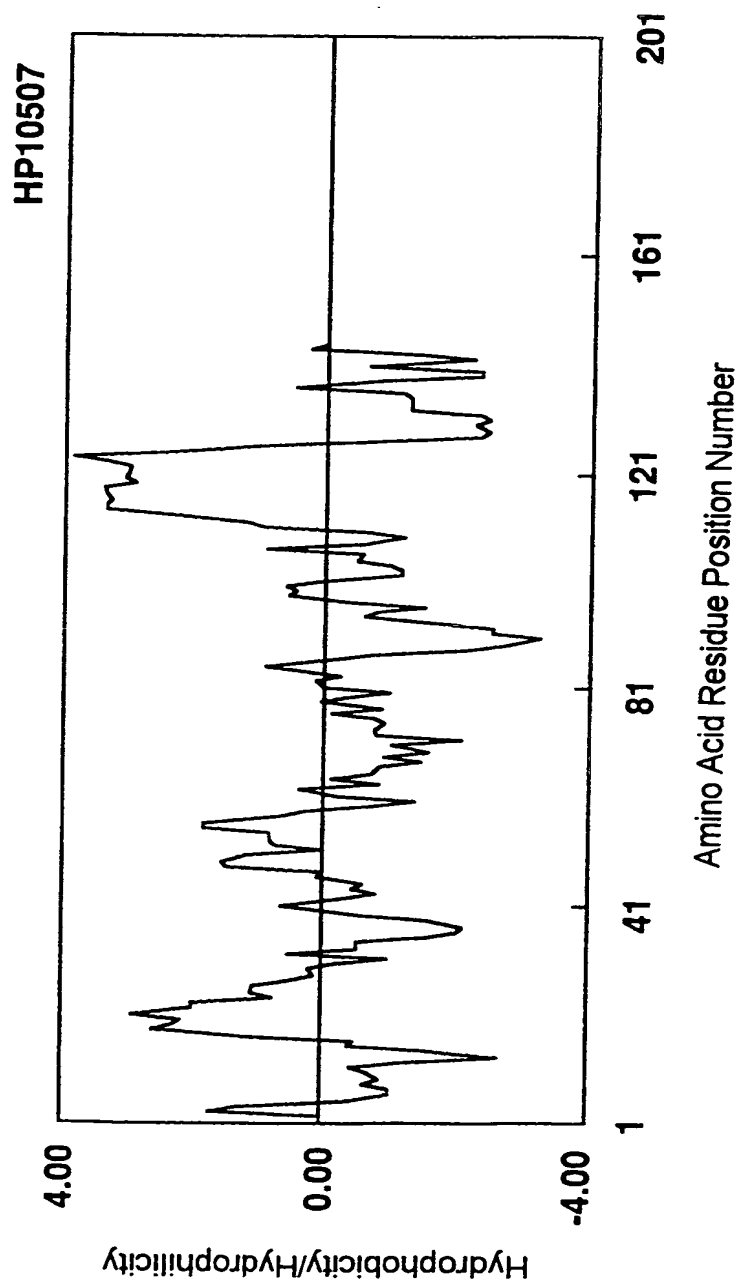


Fig. 6

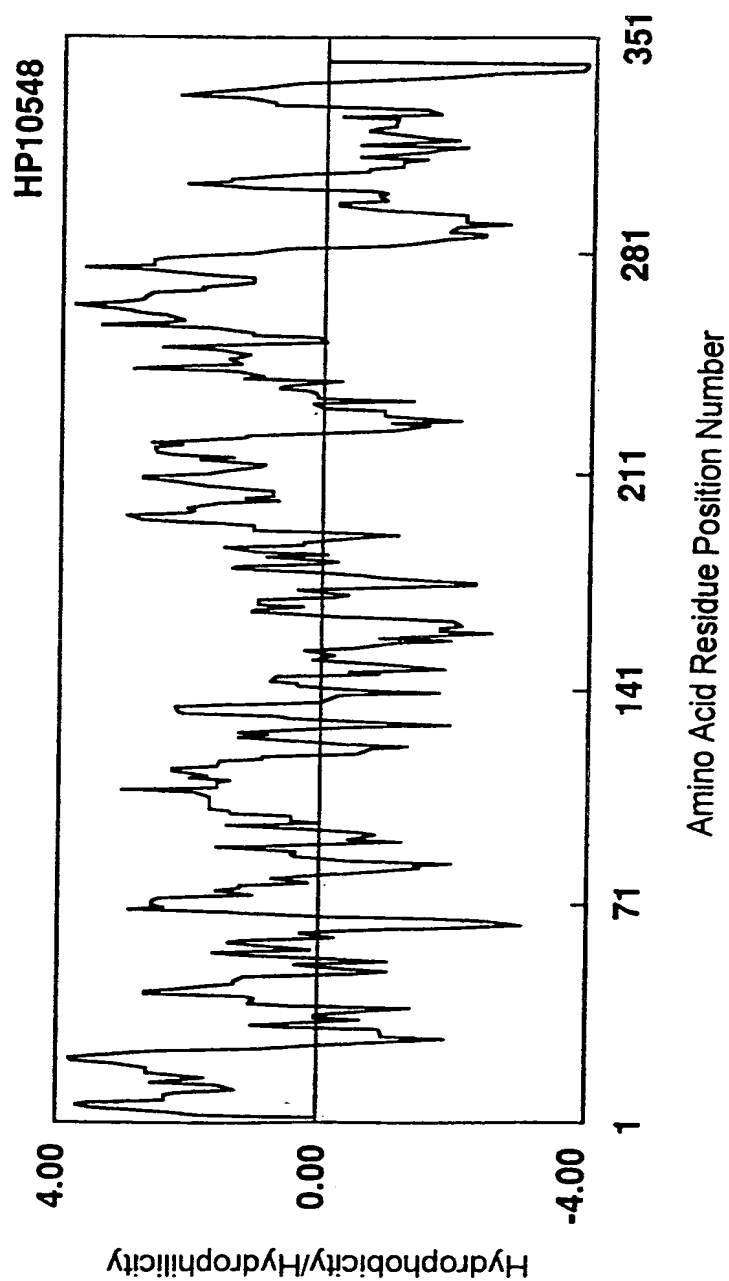


Fig. 7

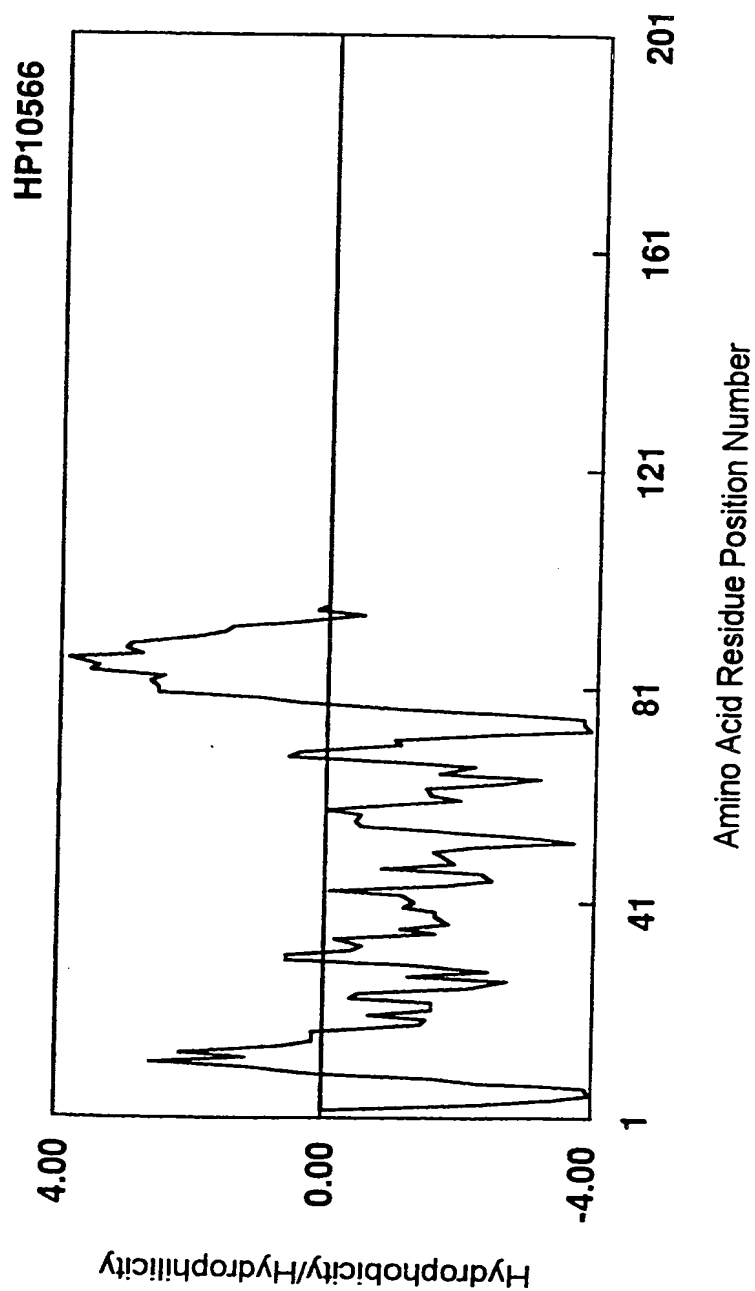


Fig. 8

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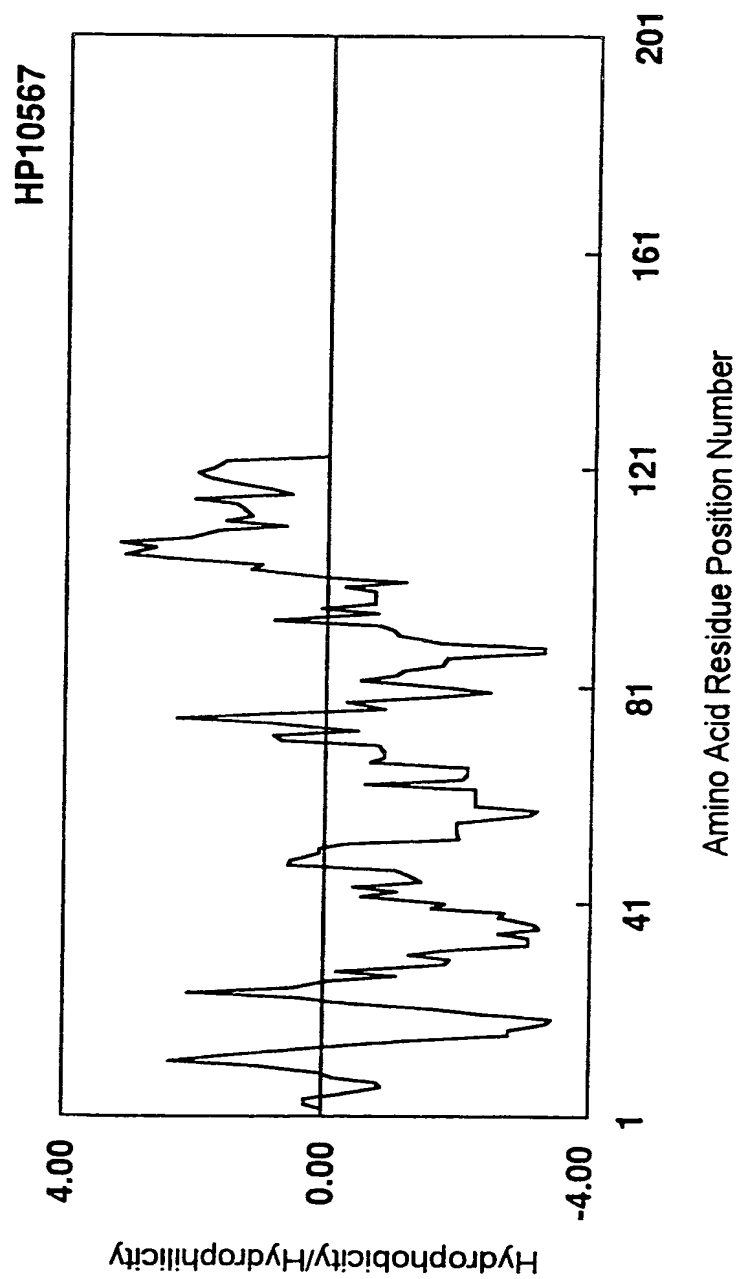


Fig. 9

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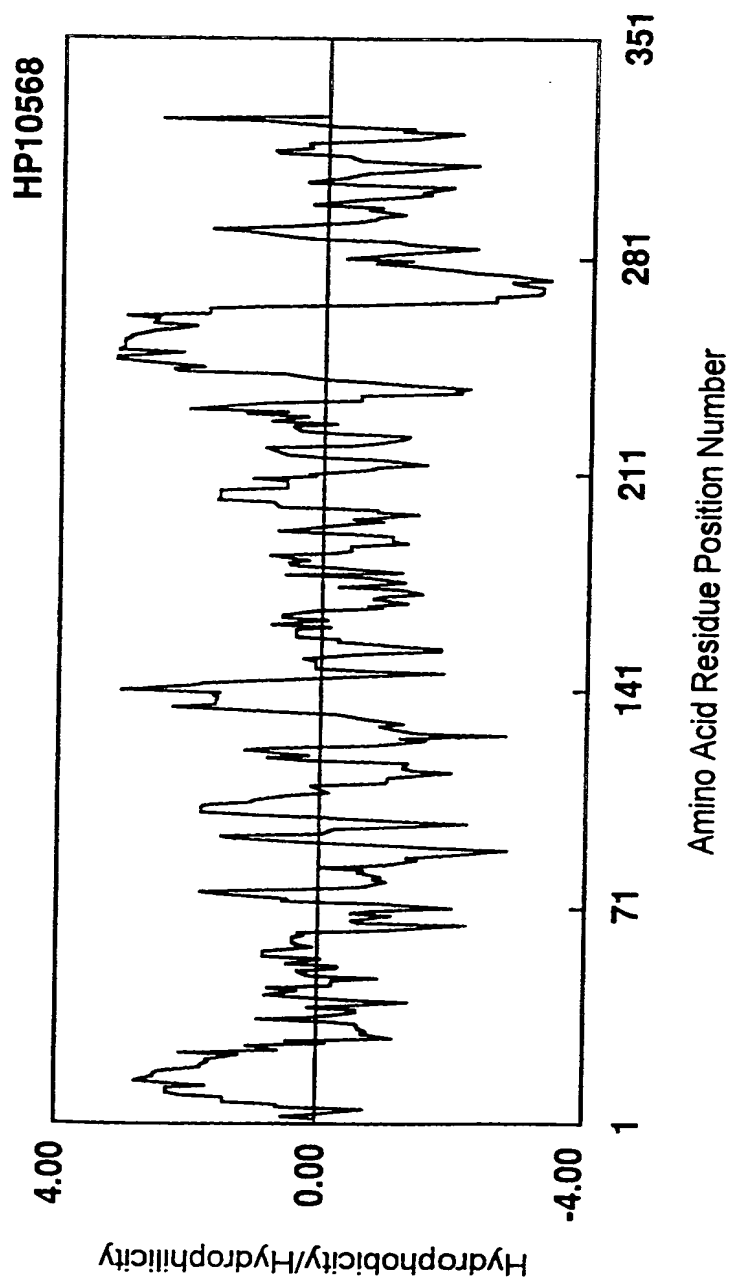


Fig. 10

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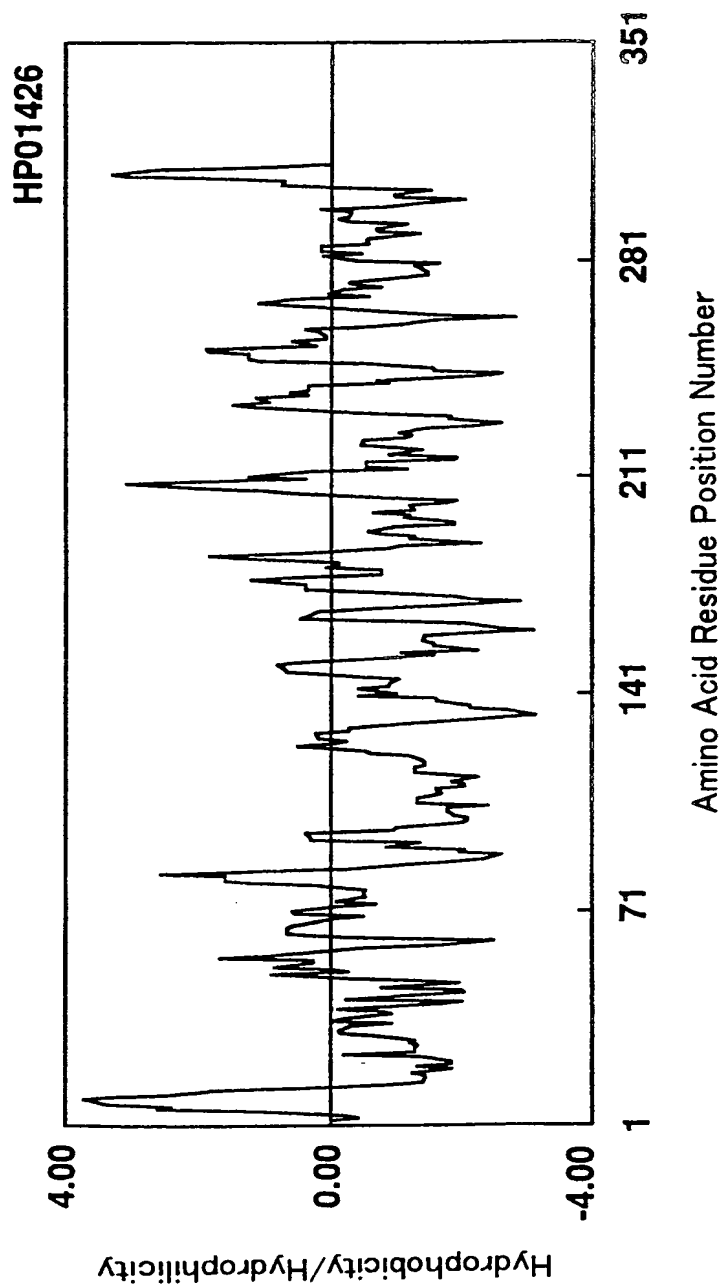


Fig. 11

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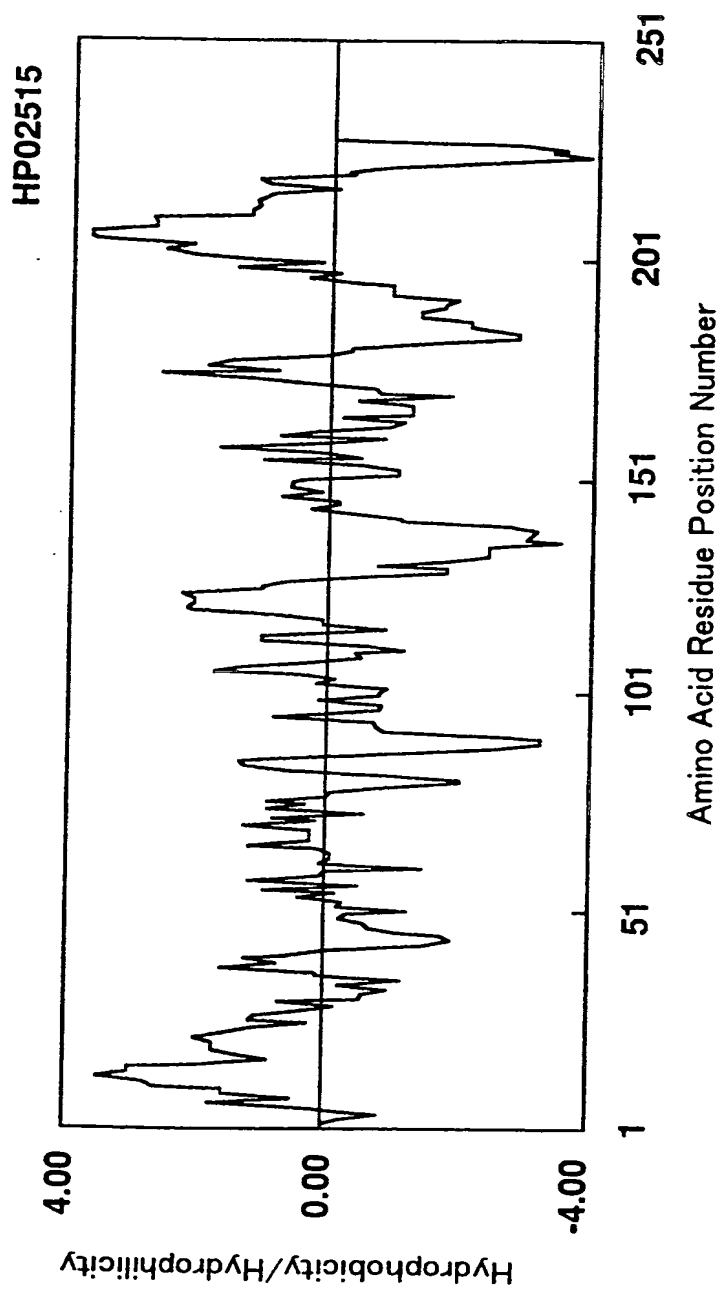


Fig.12

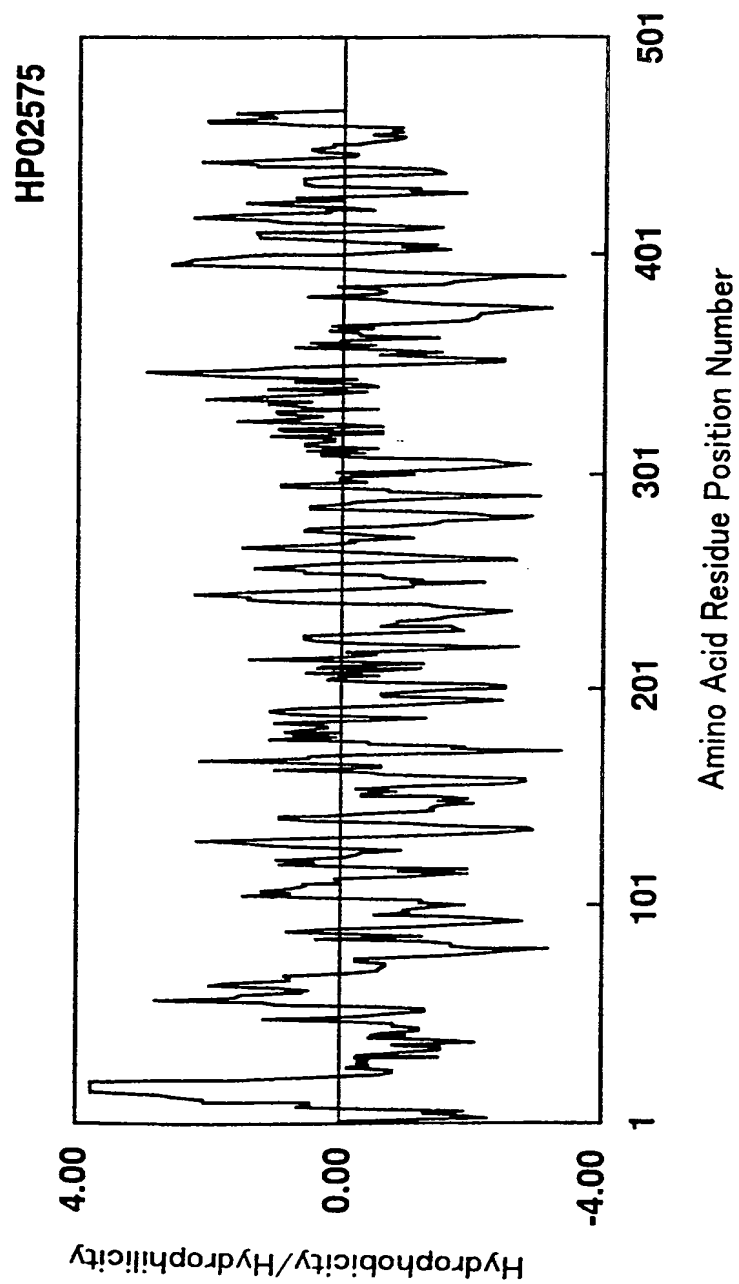


Fig. 13

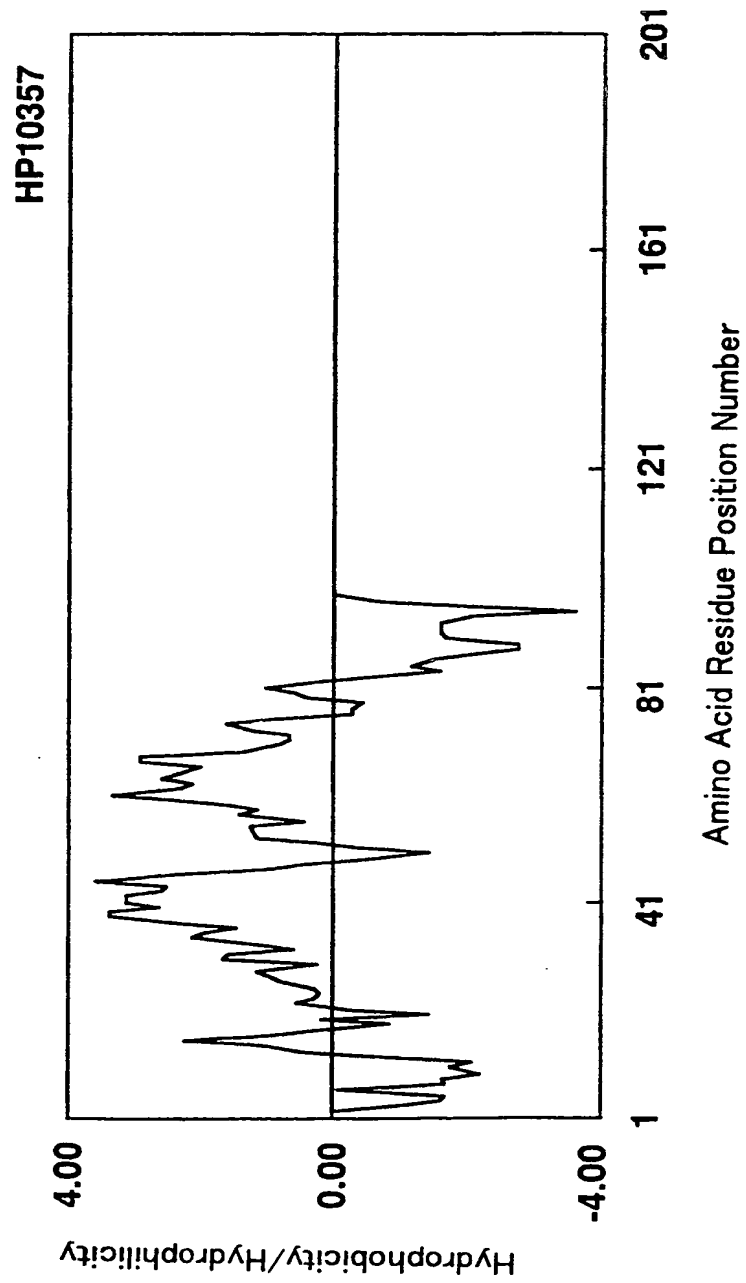


Fig. 14

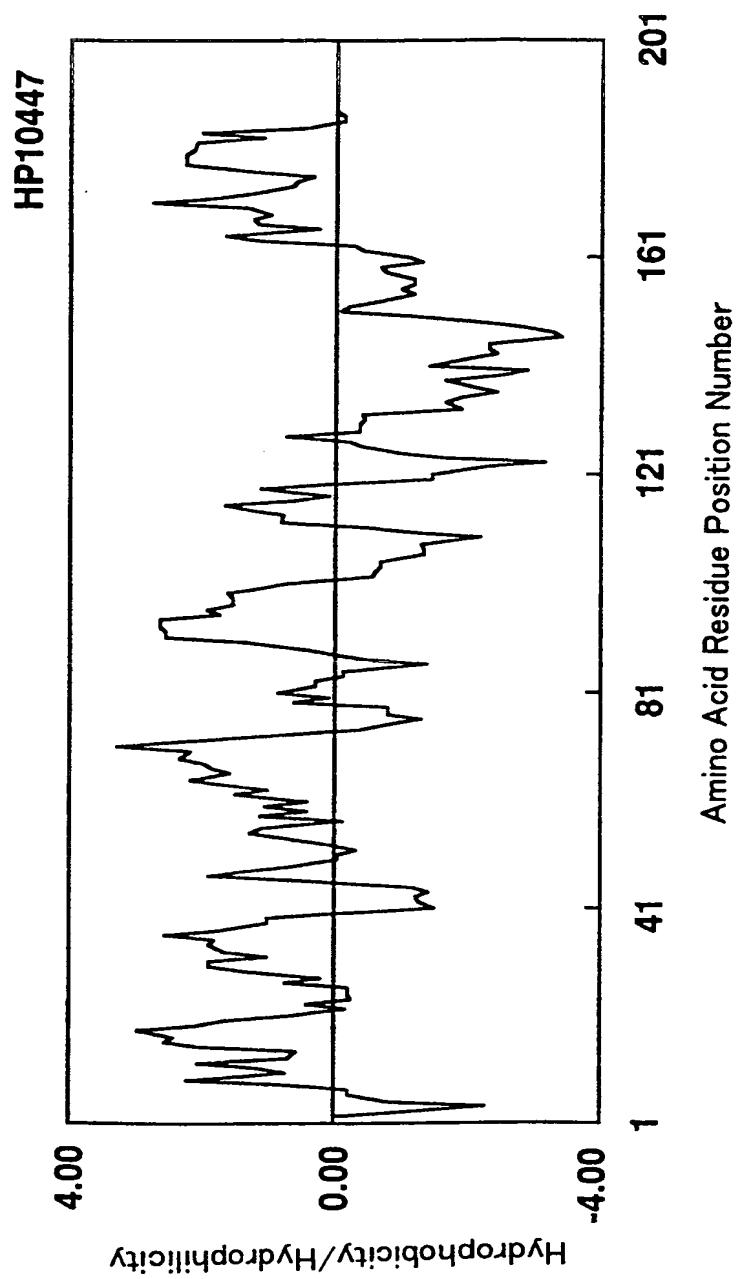


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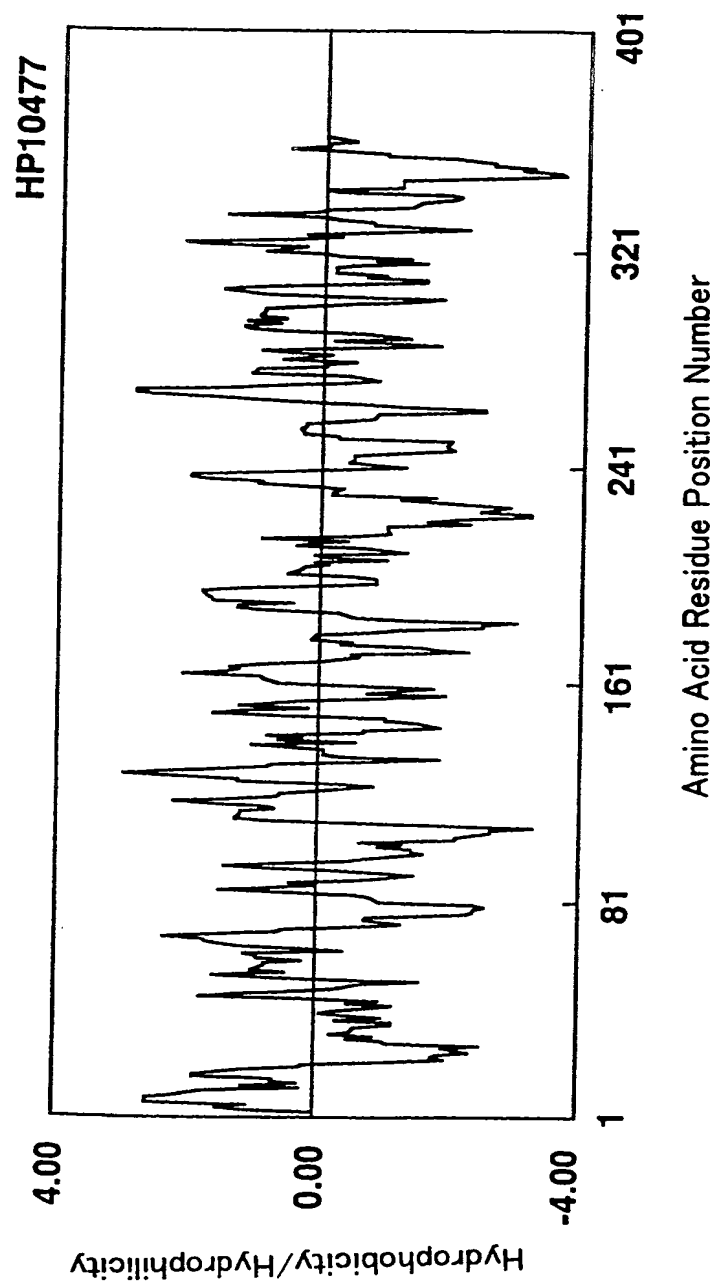


Fig. 16

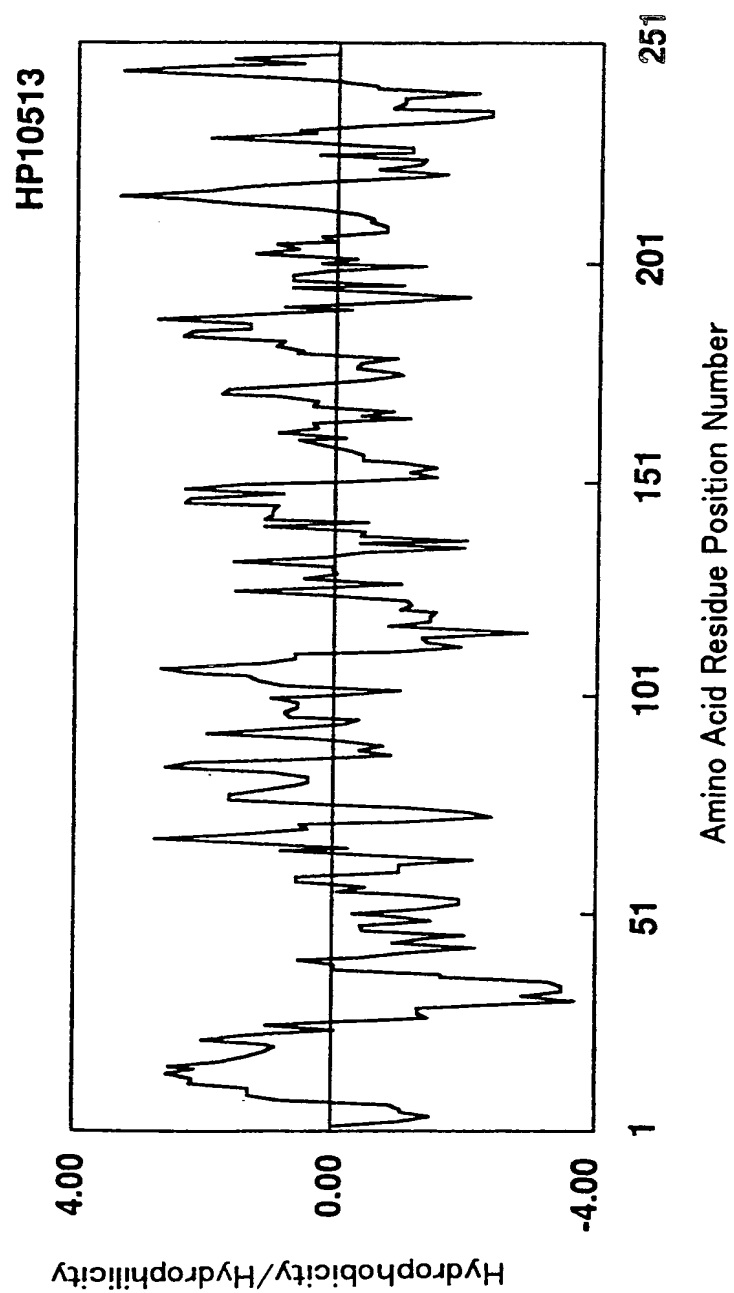


Fig.17

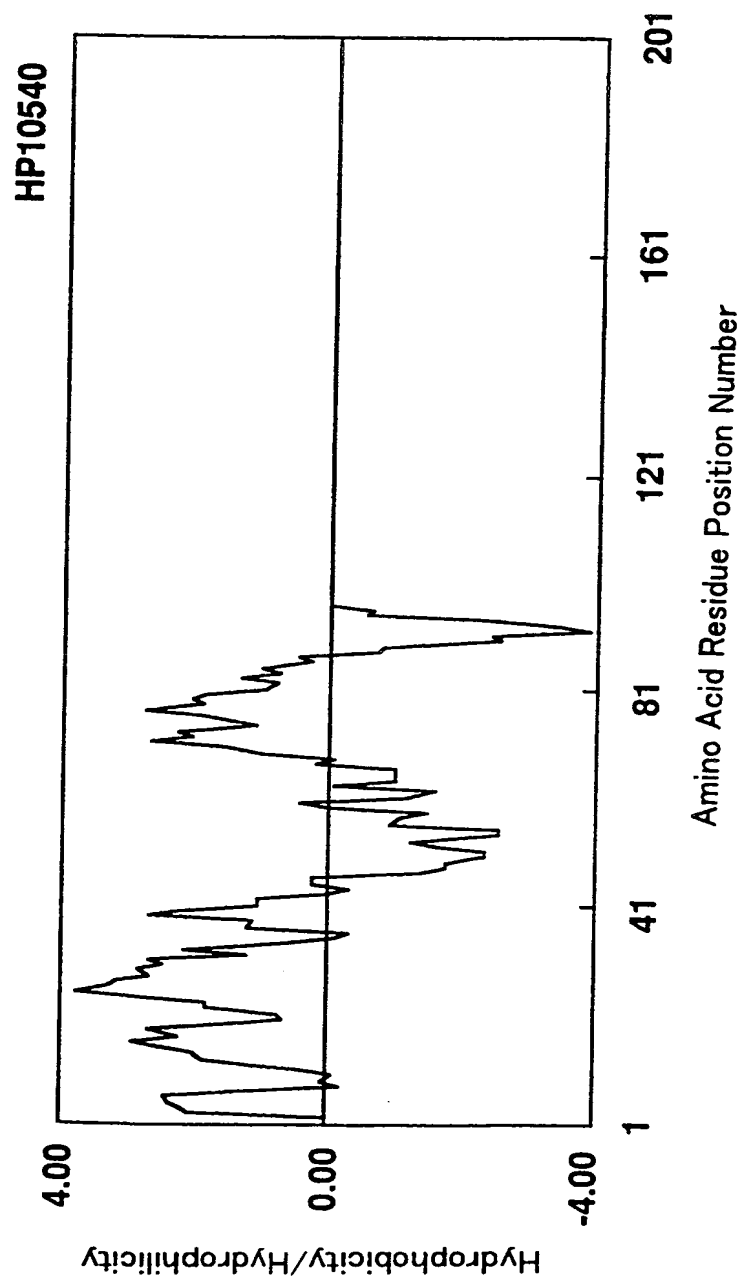


Fig. 18

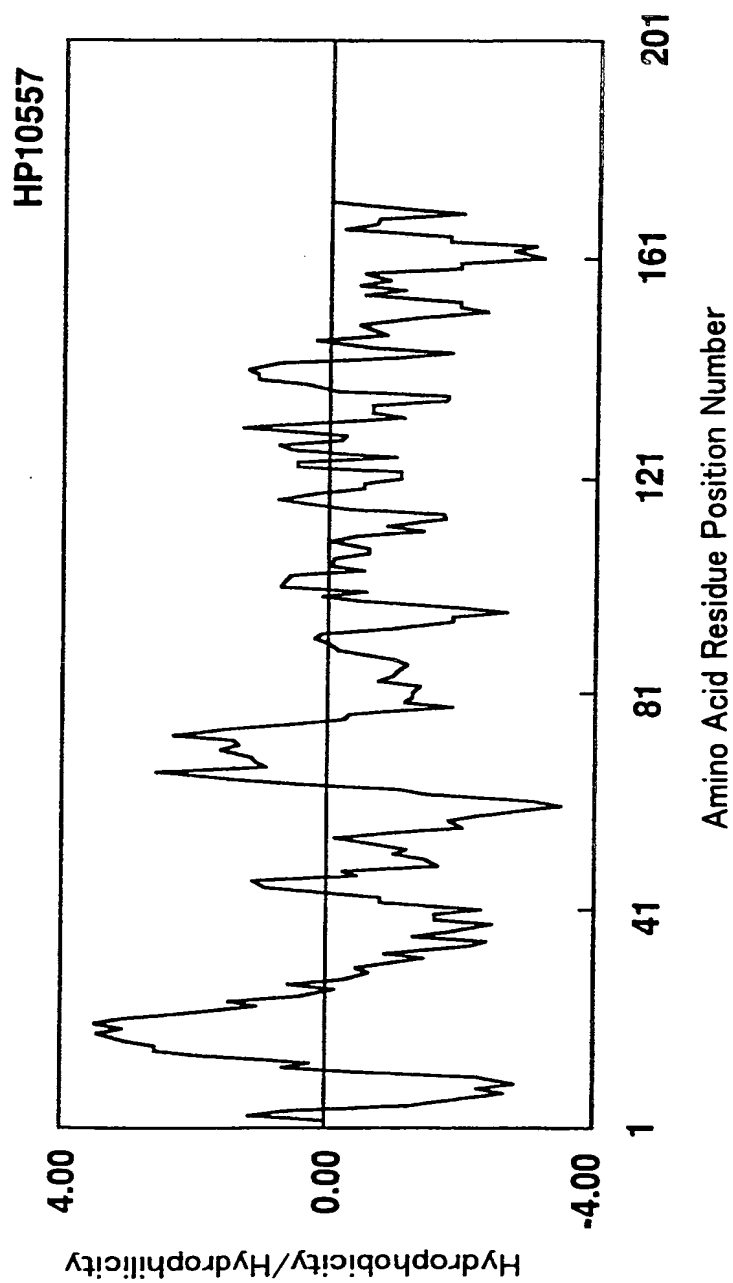


Fig. 19

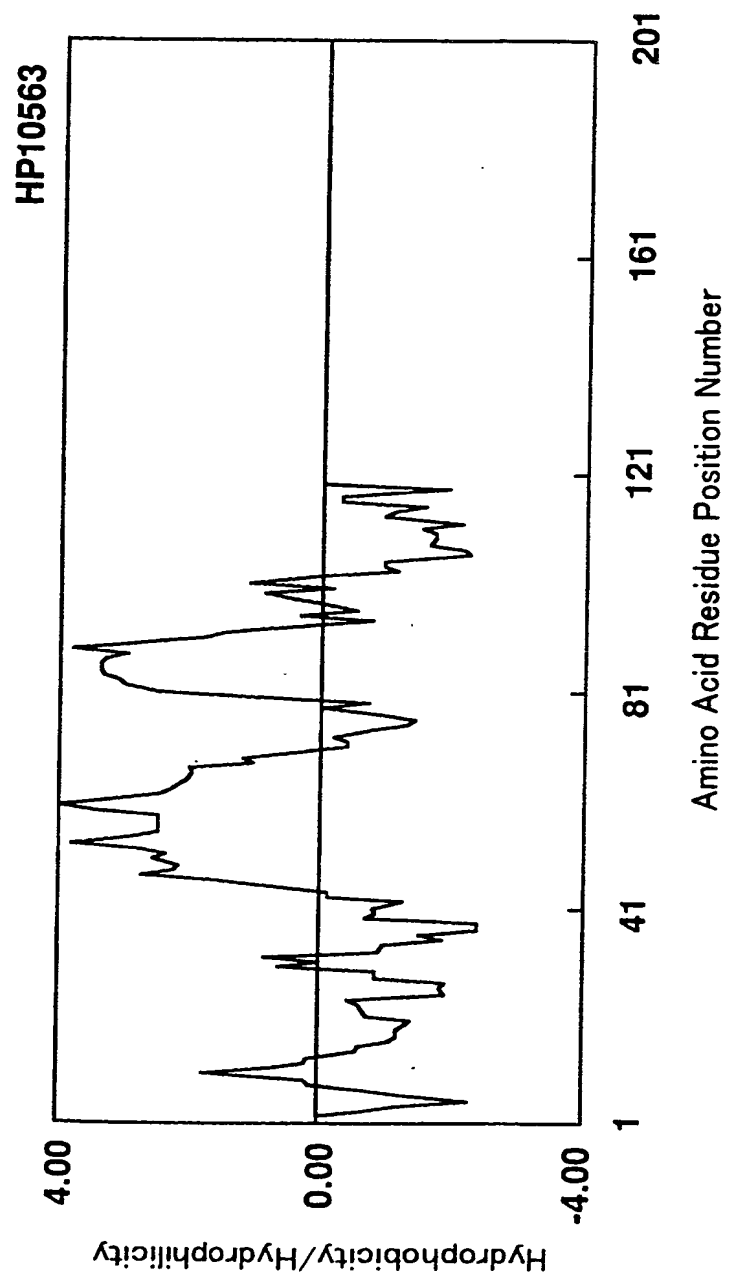


Fig. 20

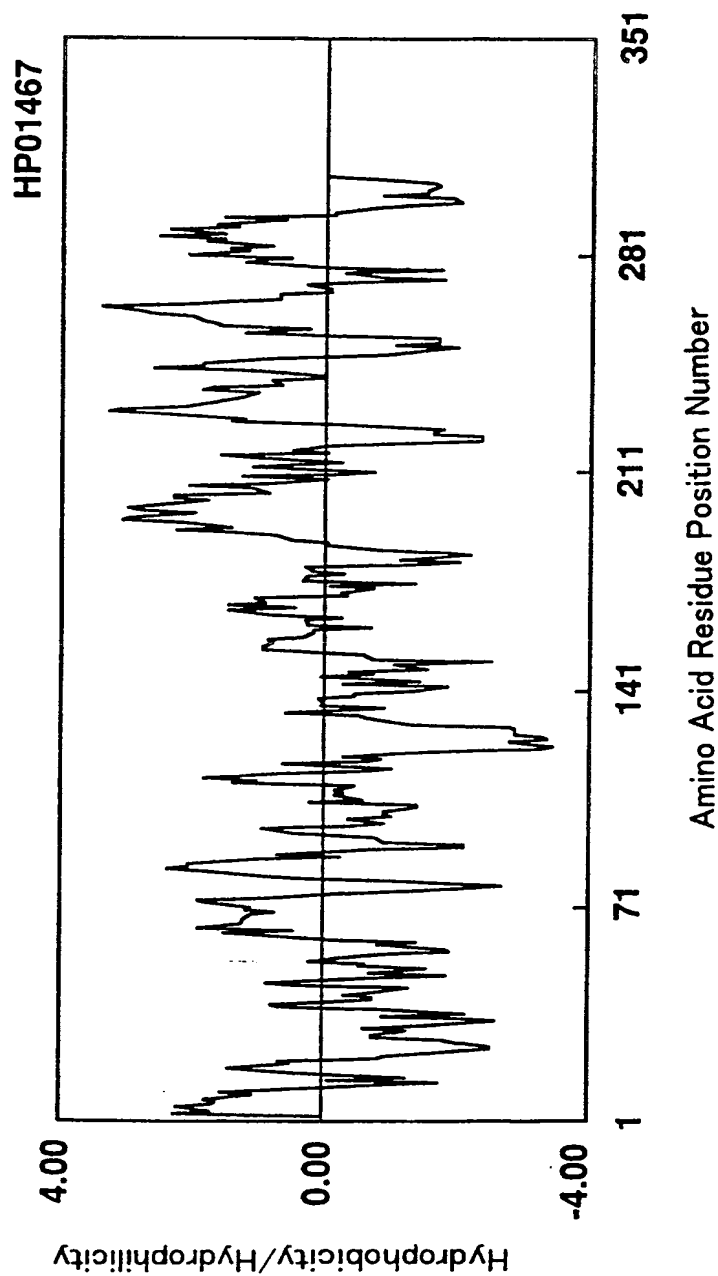


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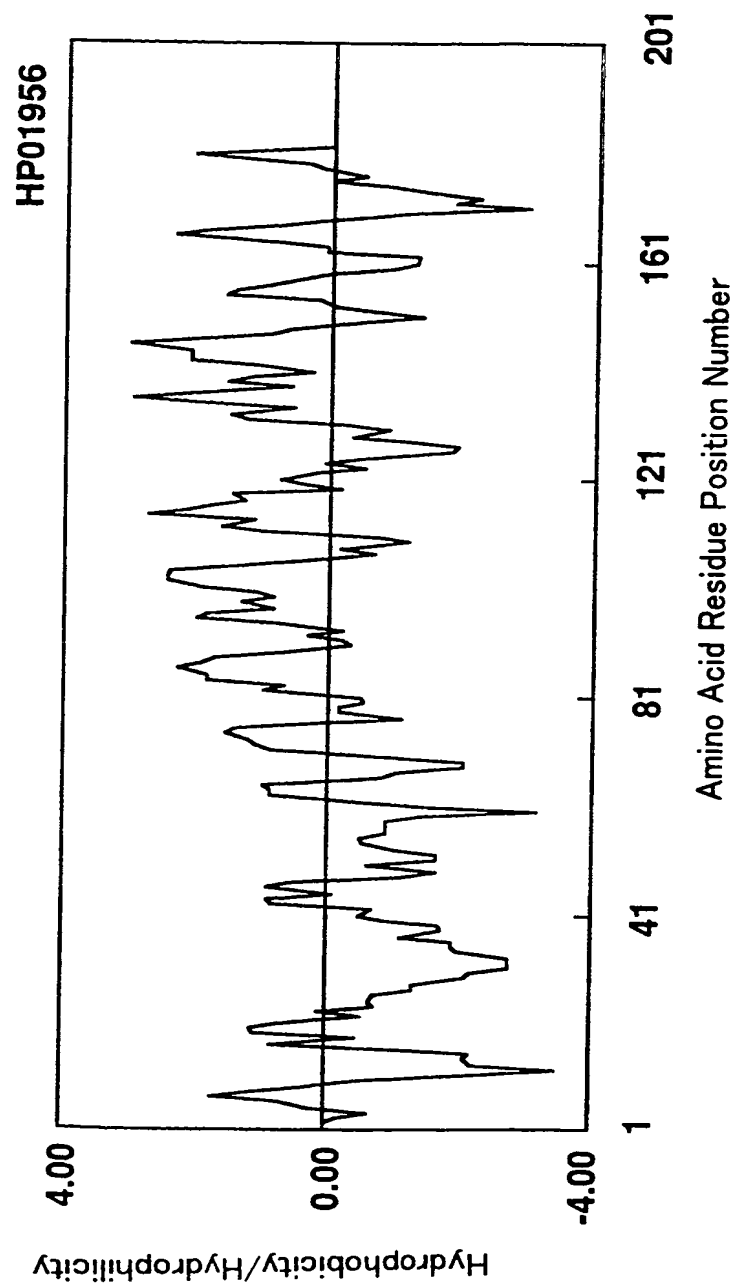


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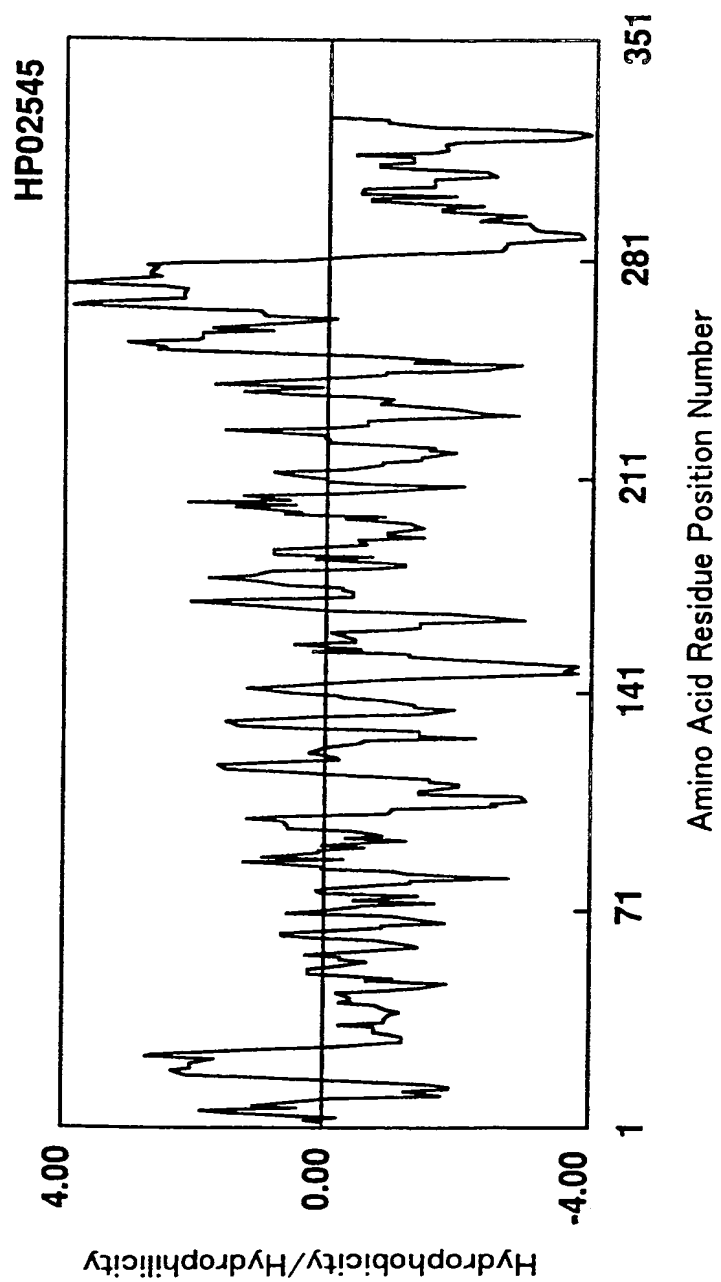


Fig. 23

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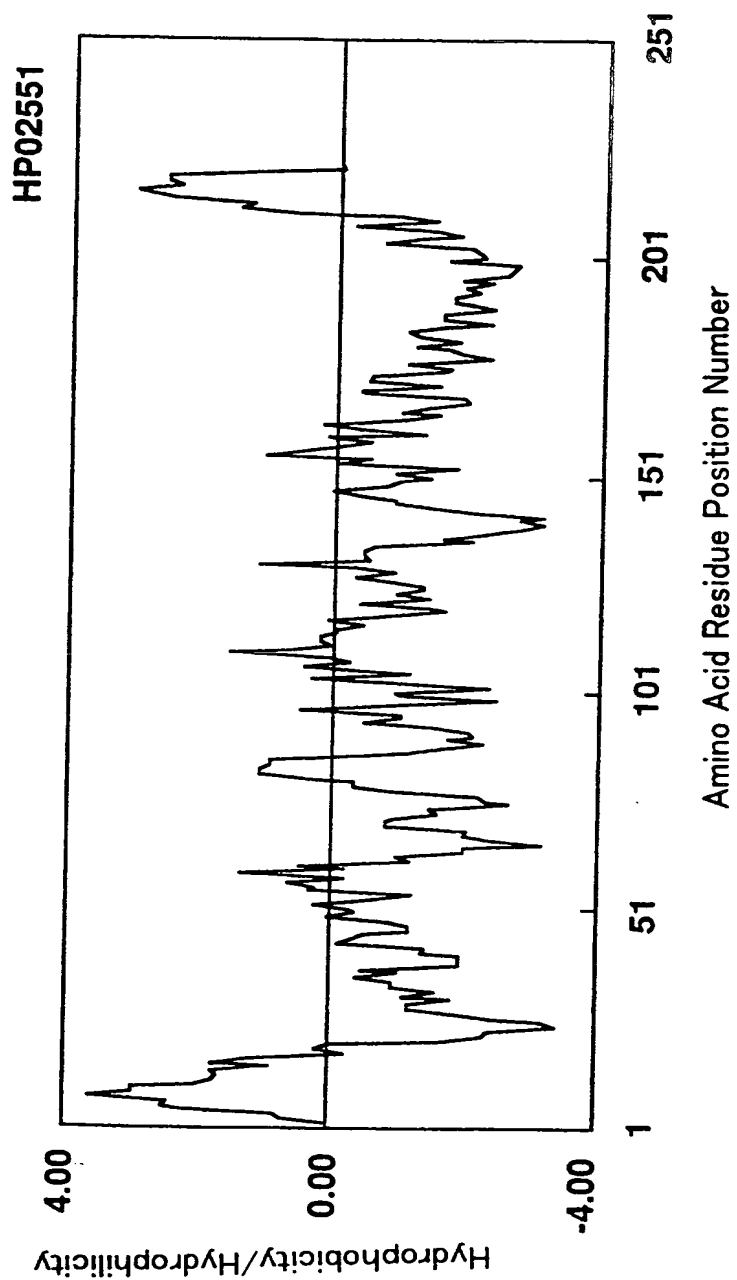


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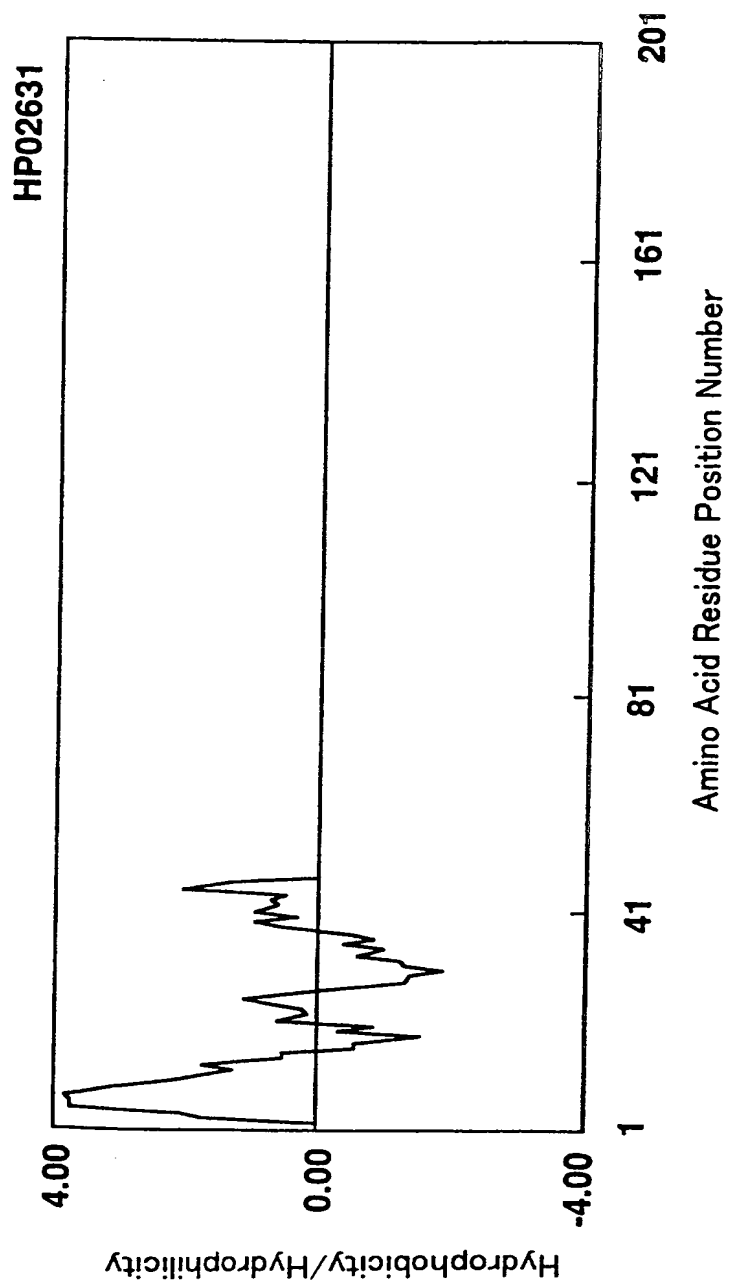


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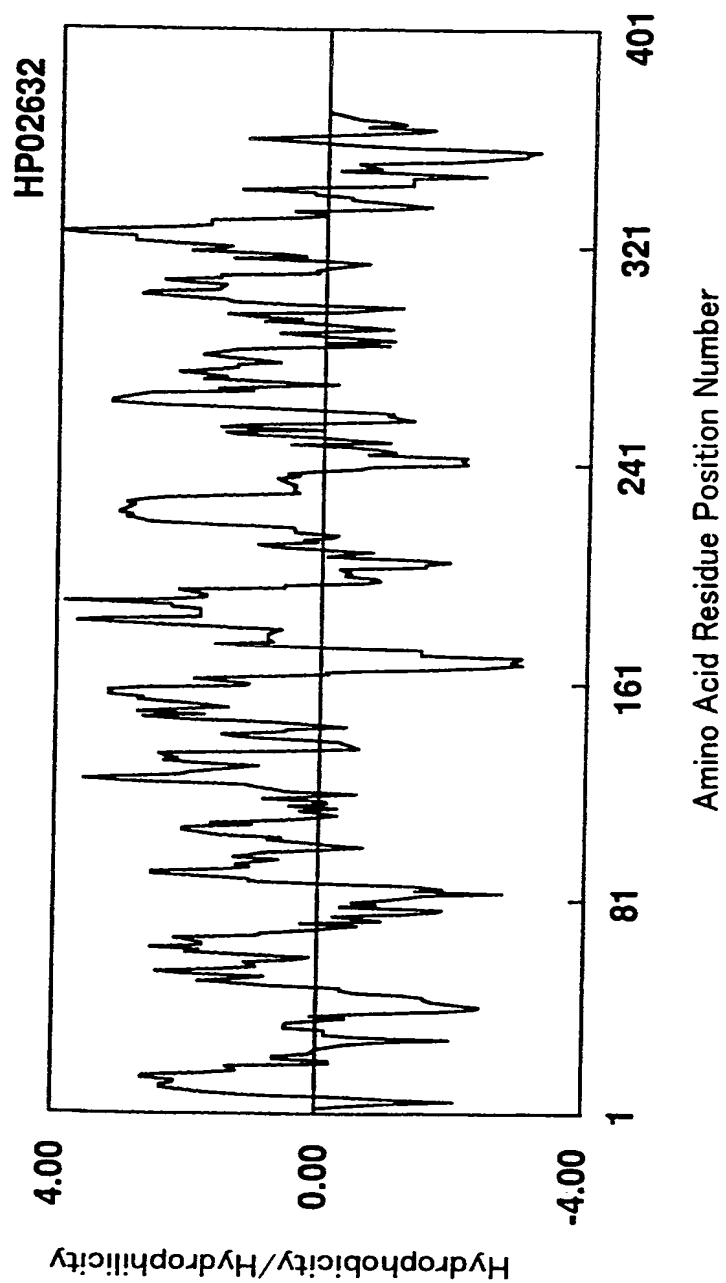


Fig. 26

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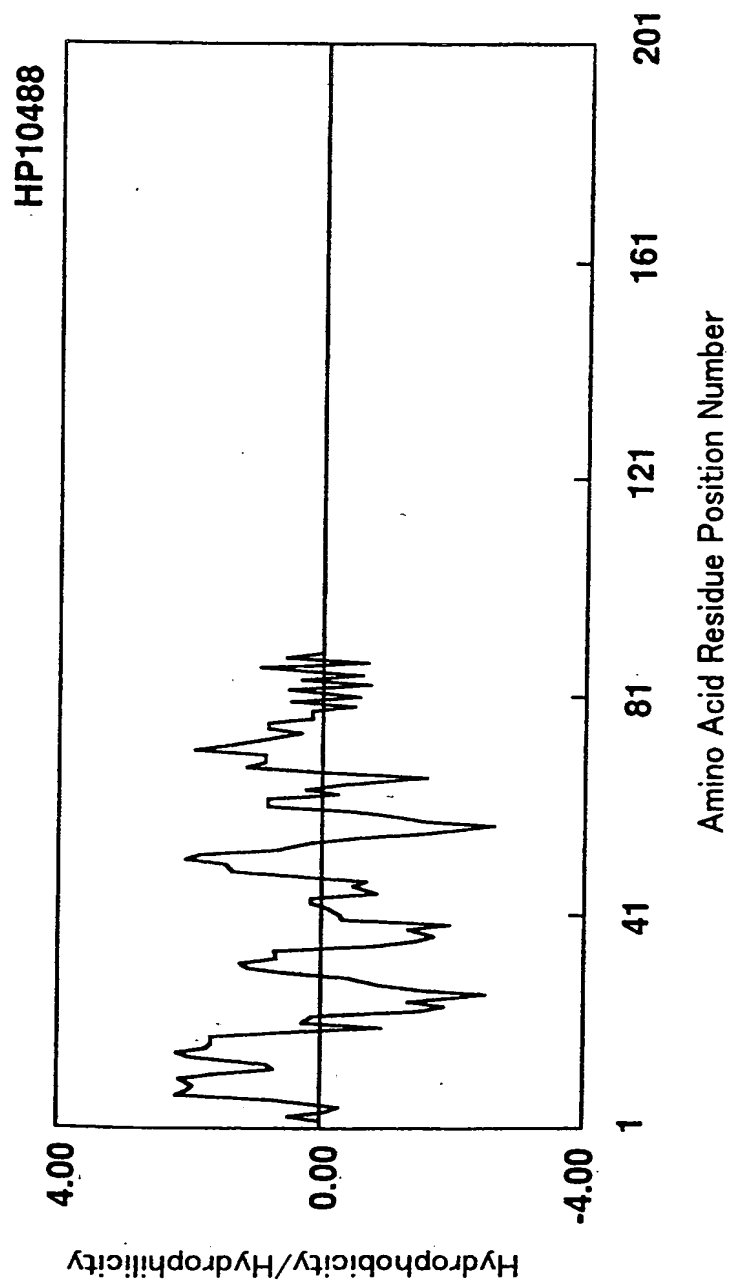


Fig.27

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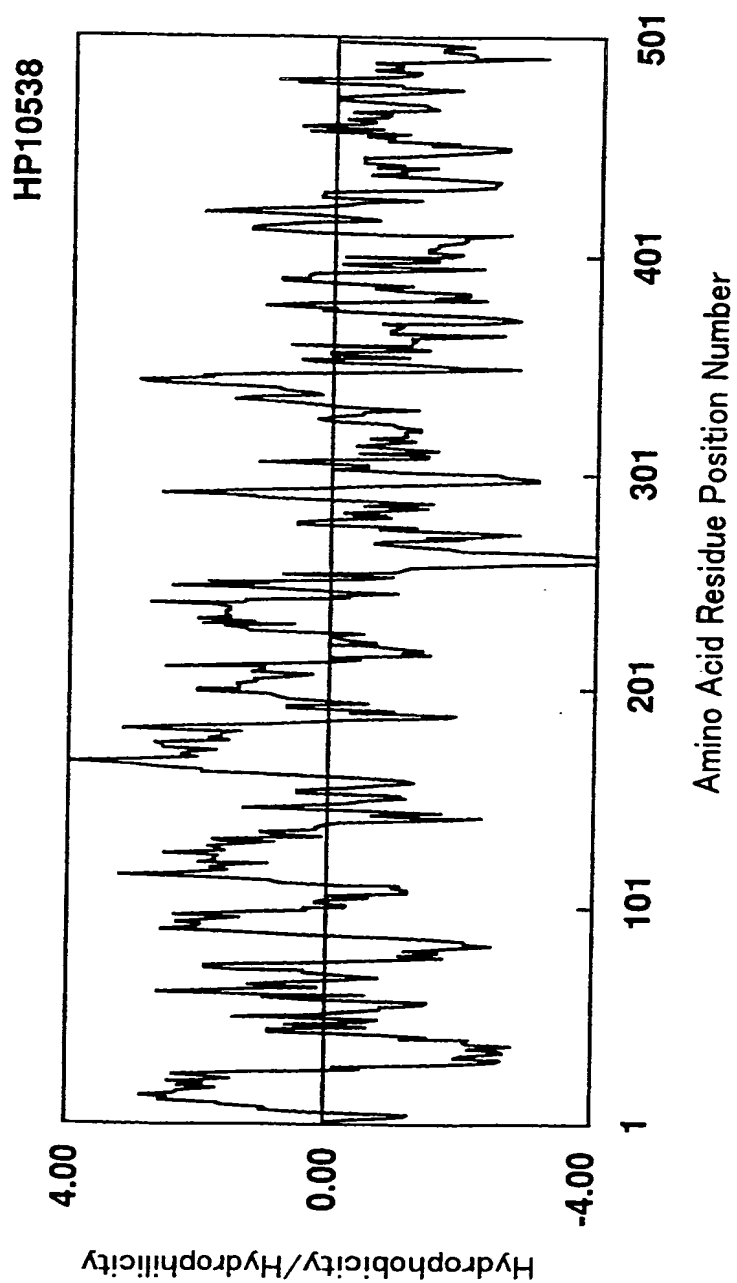


Fig. 28

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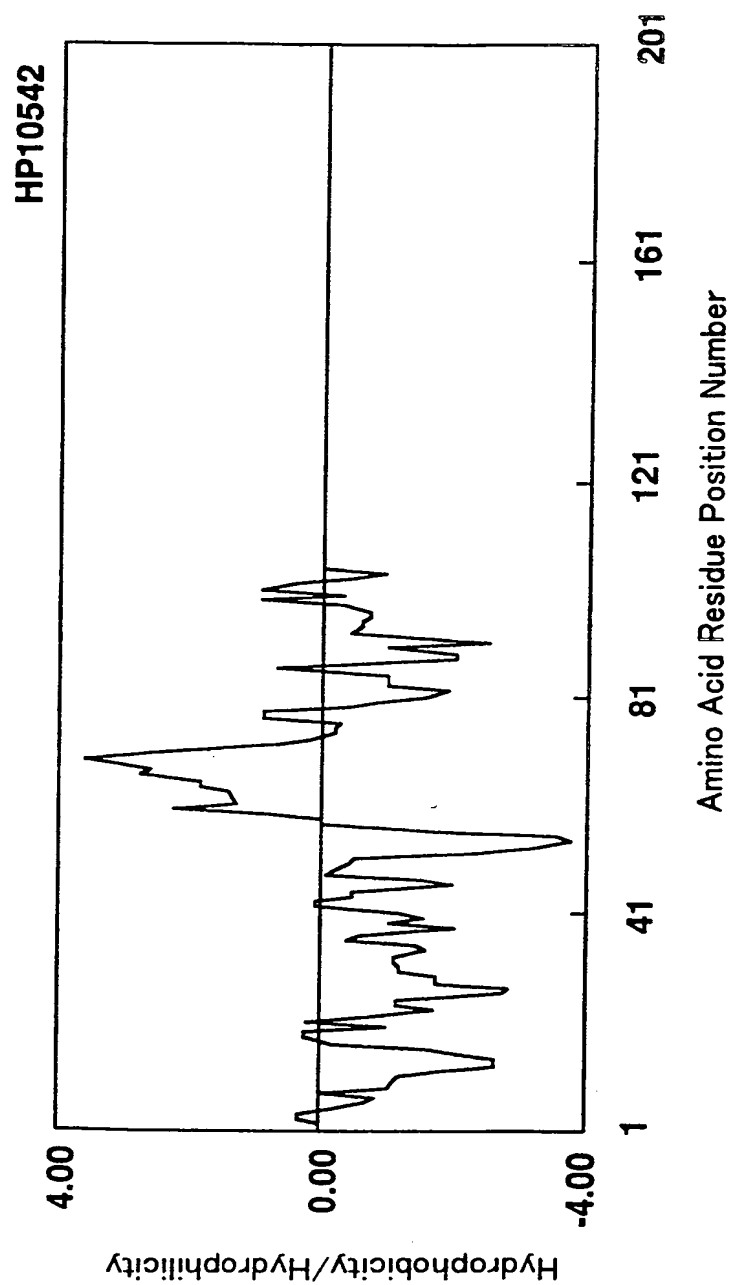


Fig. 29

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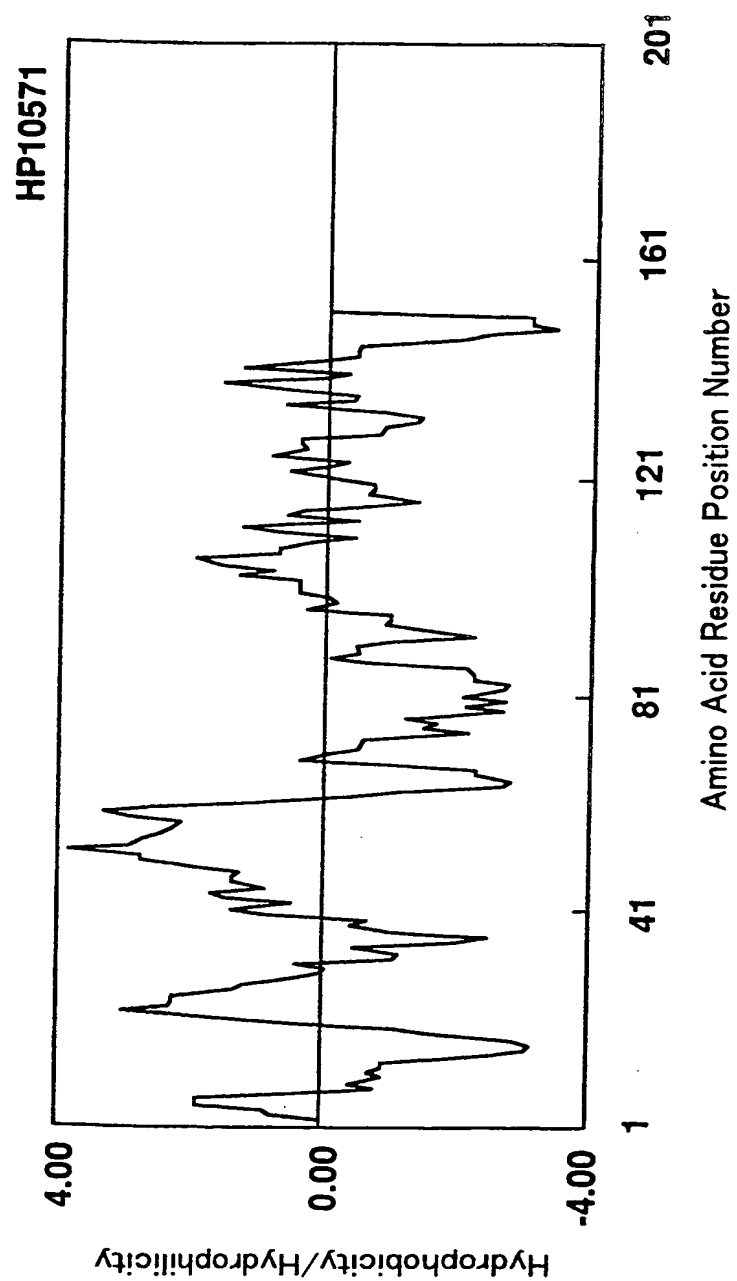


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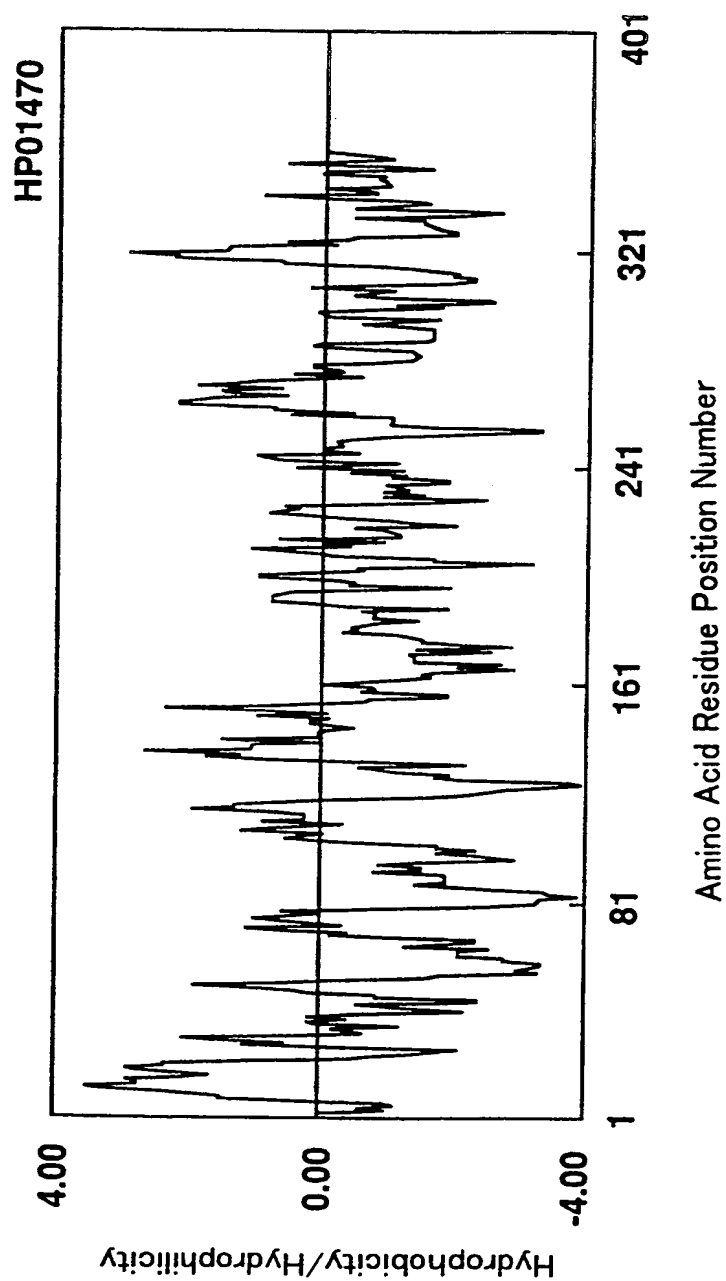


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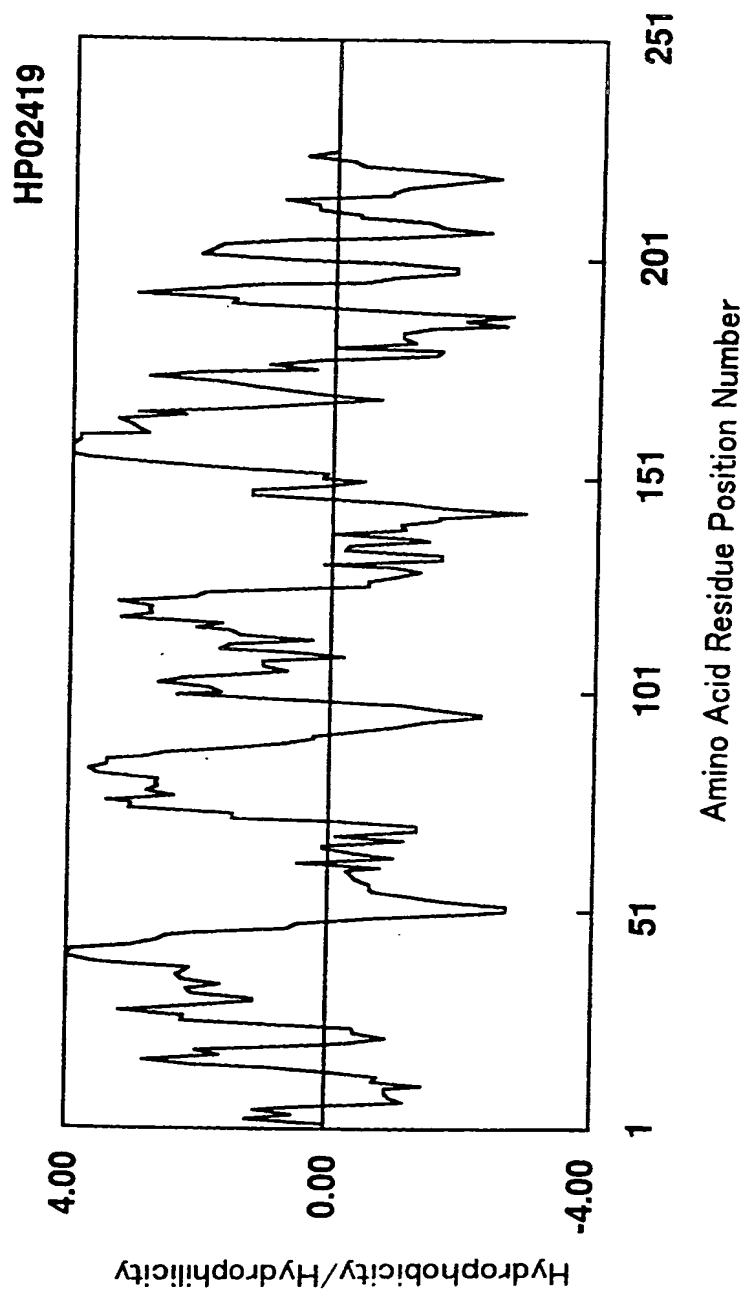


Fig.32

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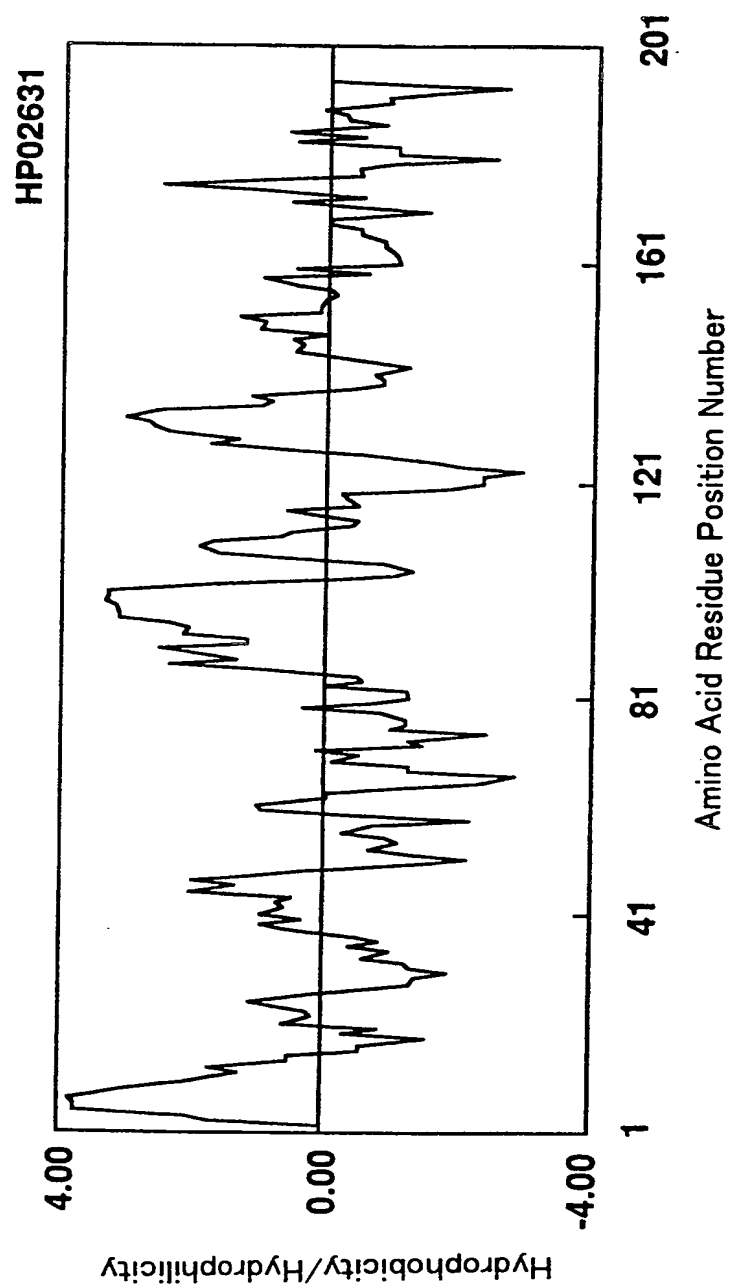


Fig. 33

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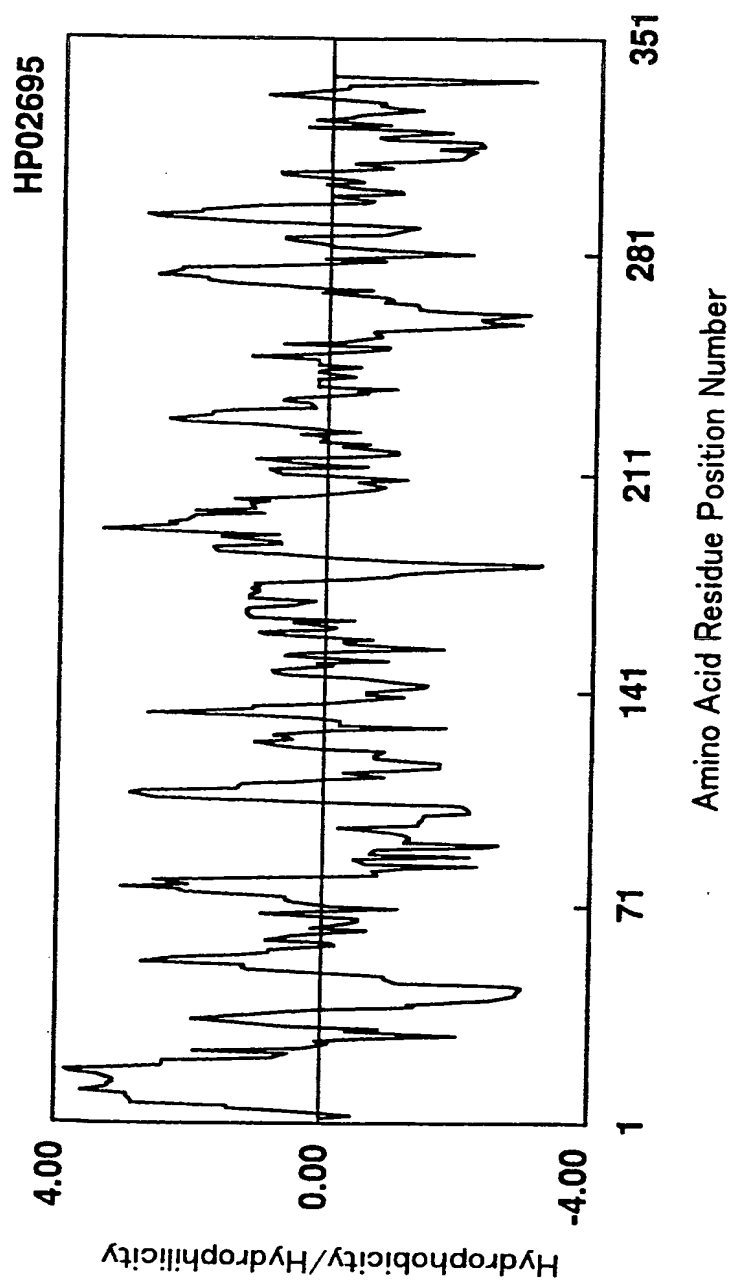


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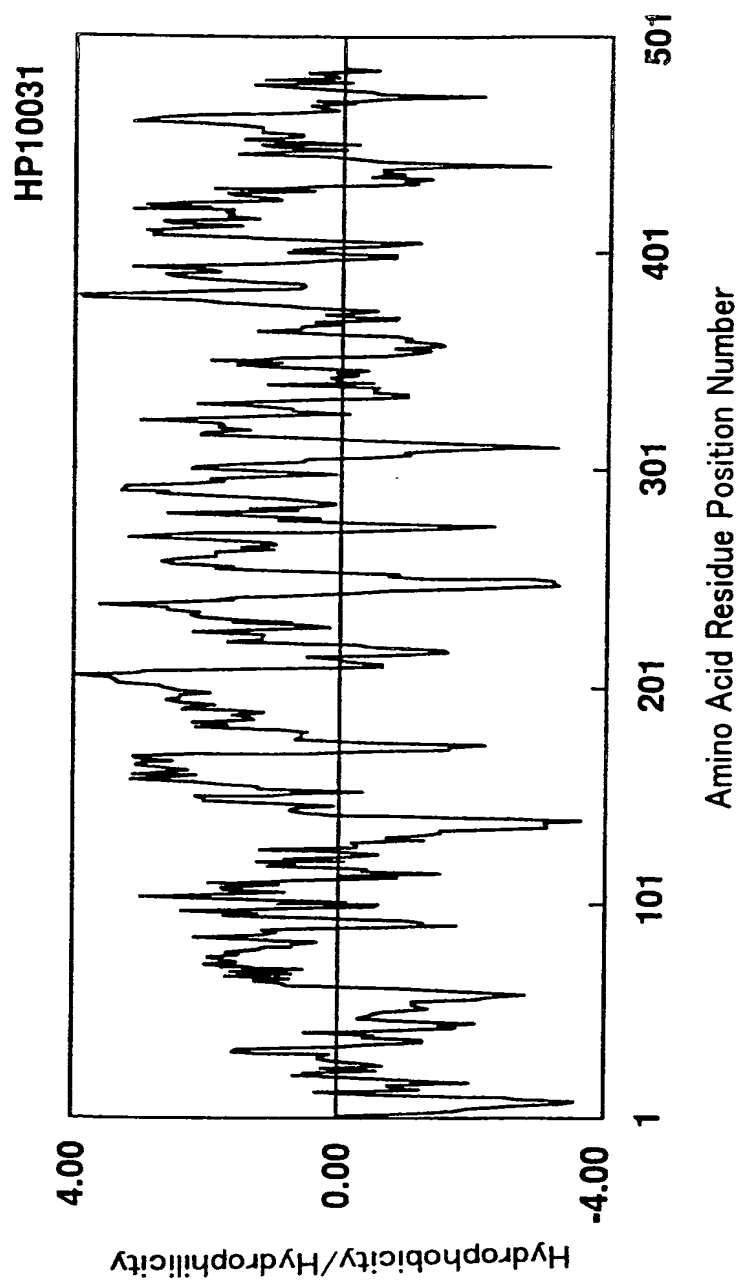


Fig. 35

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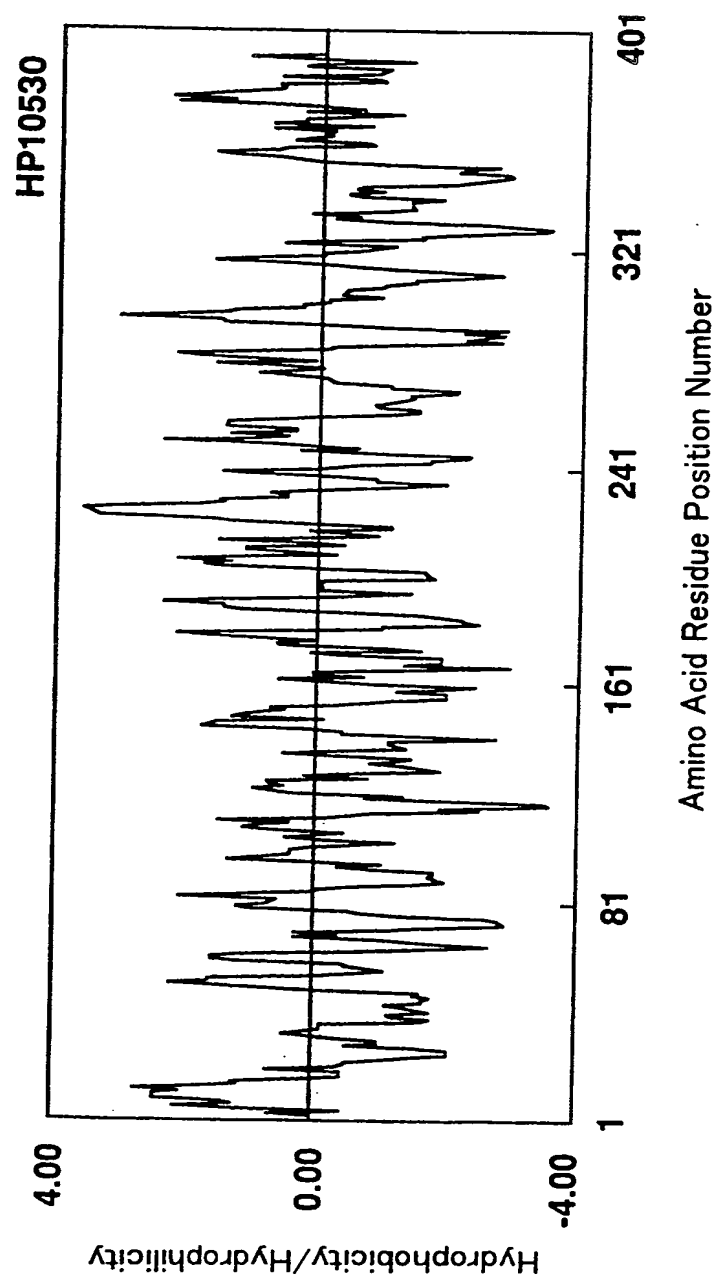


Fig. 36

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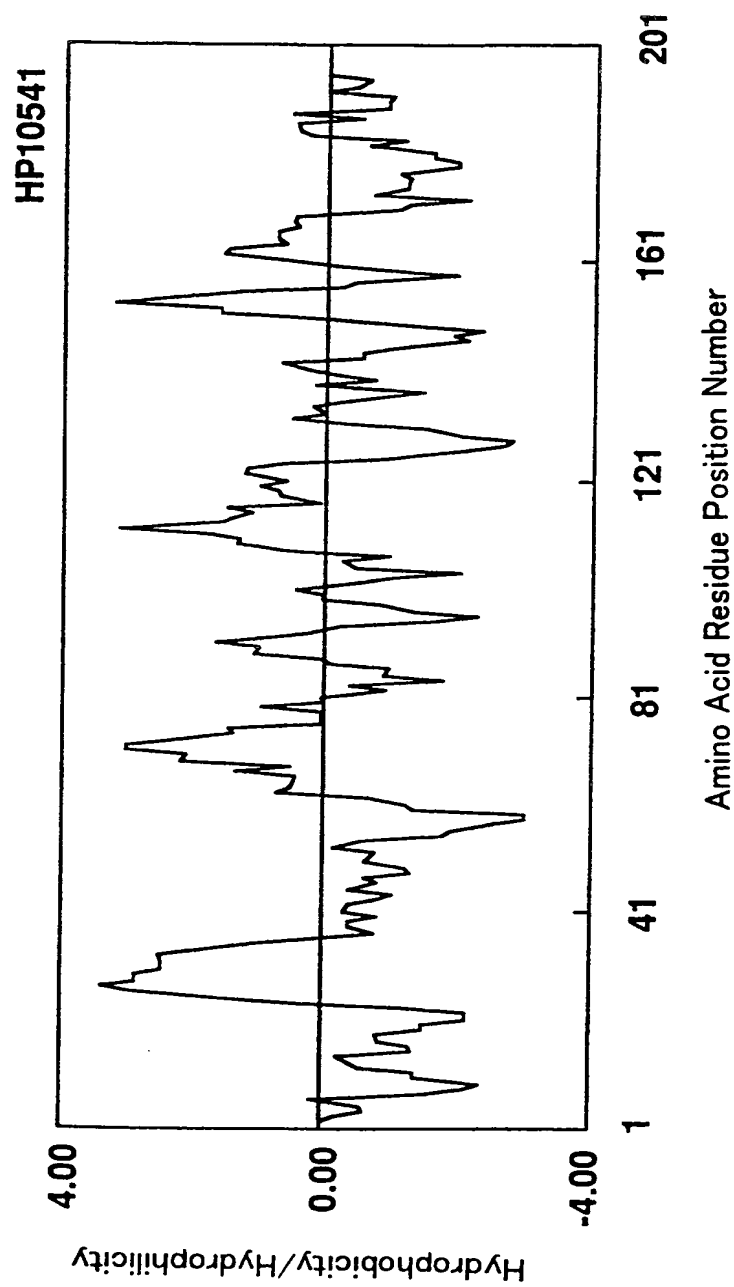


Fig.37

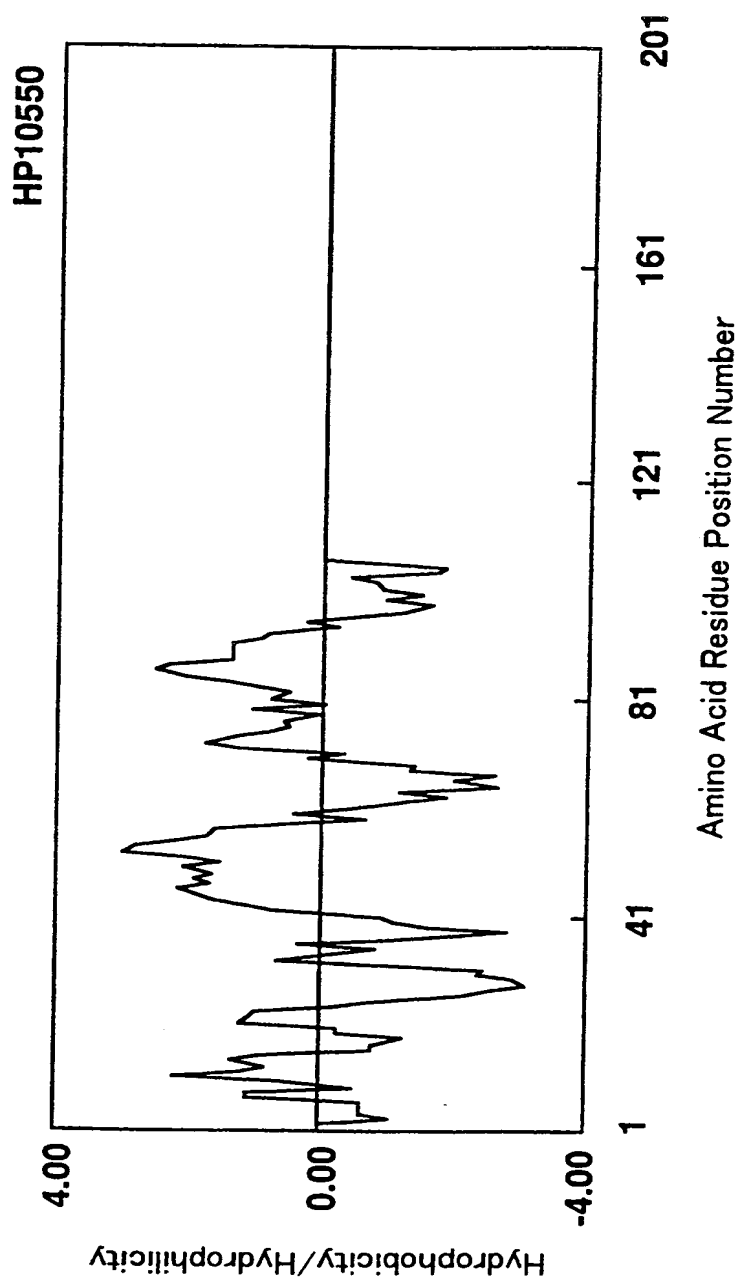


Fig. 38

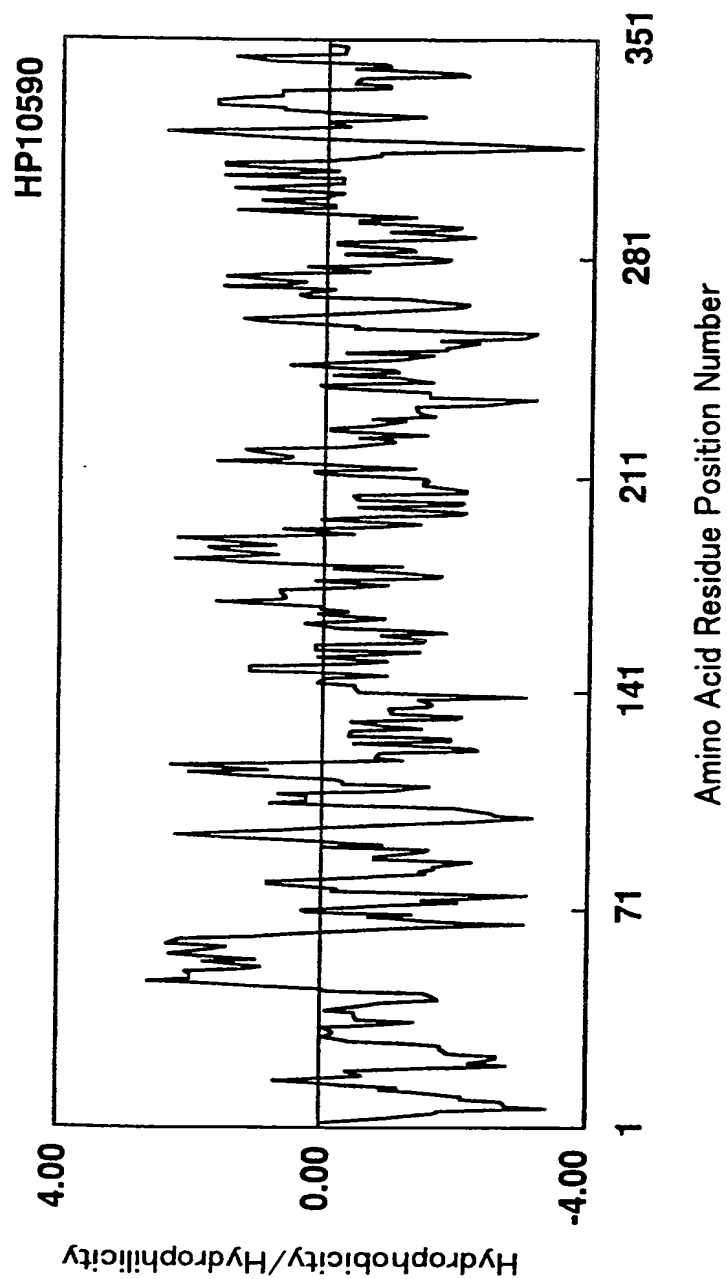


Fig. 39

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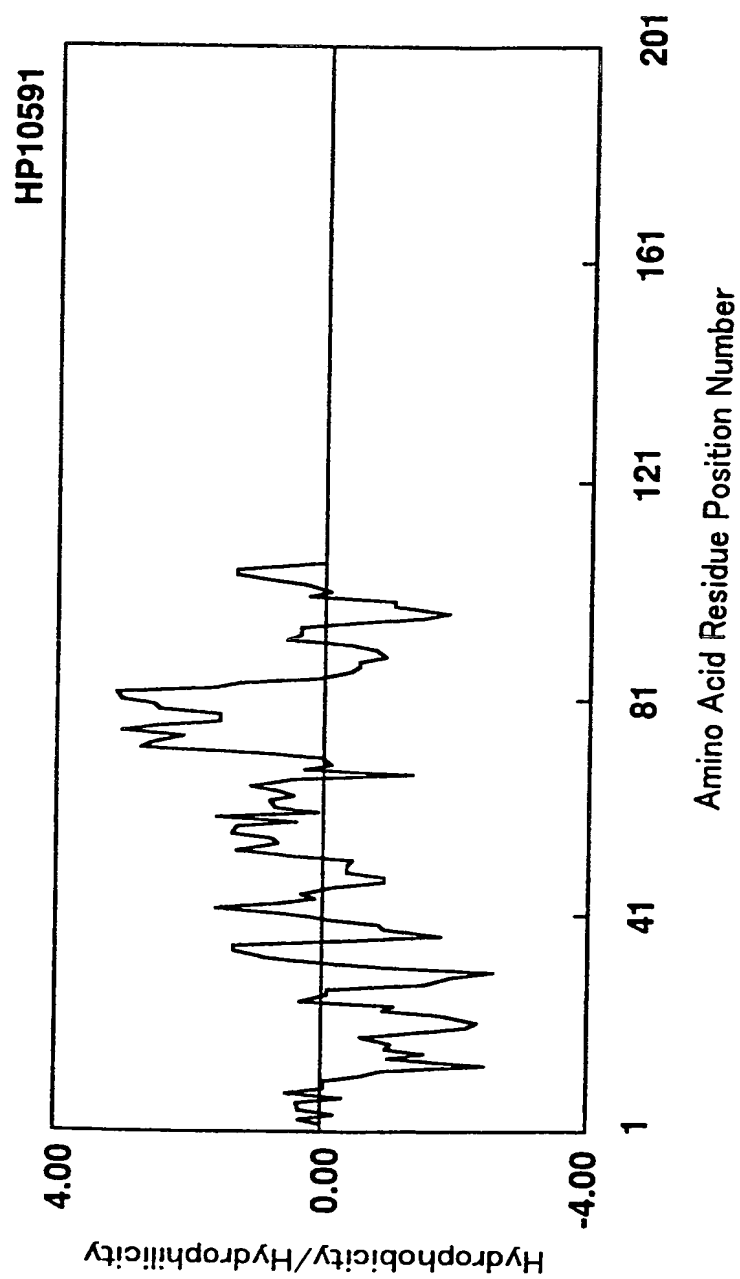


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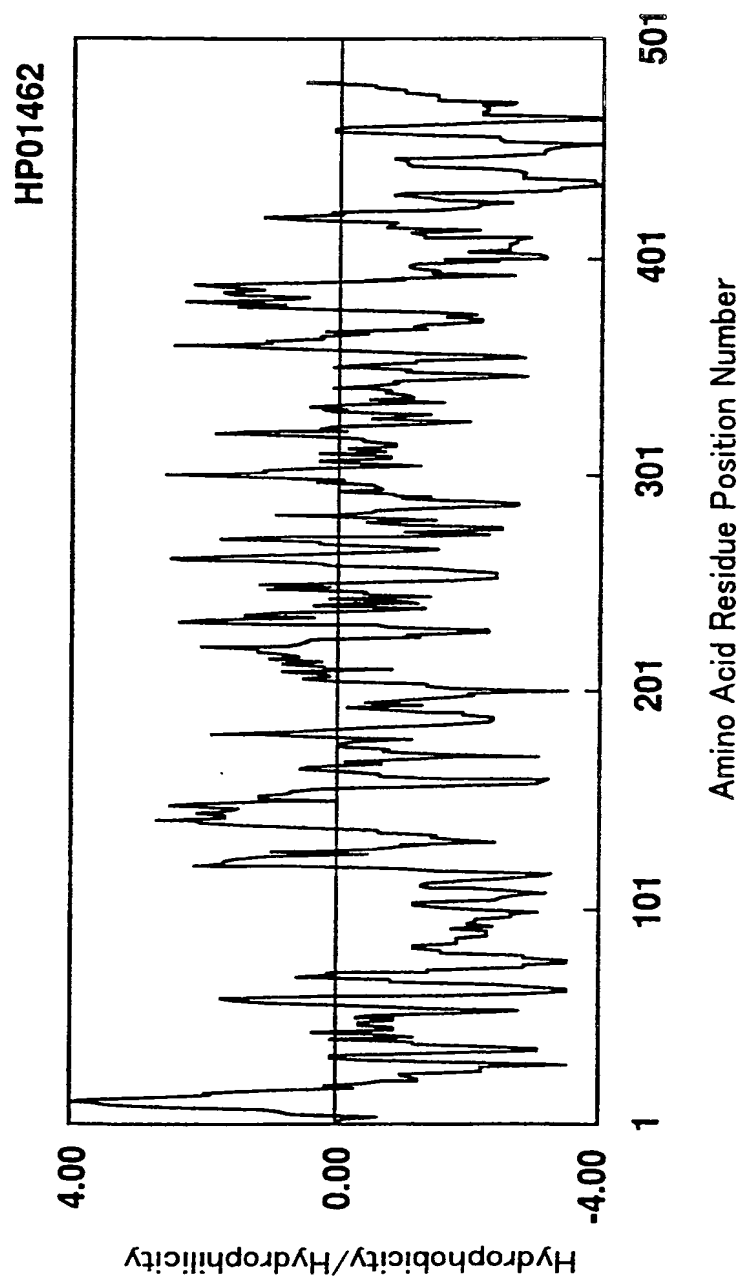


Fig. 41

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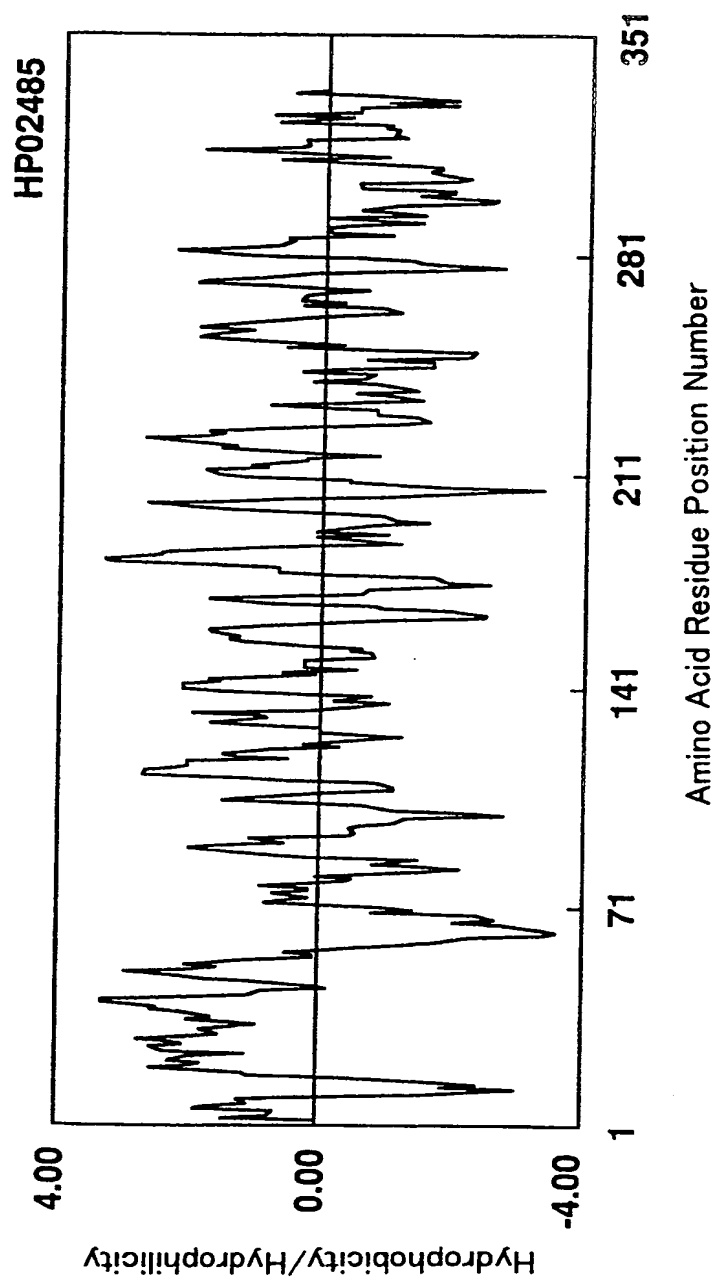


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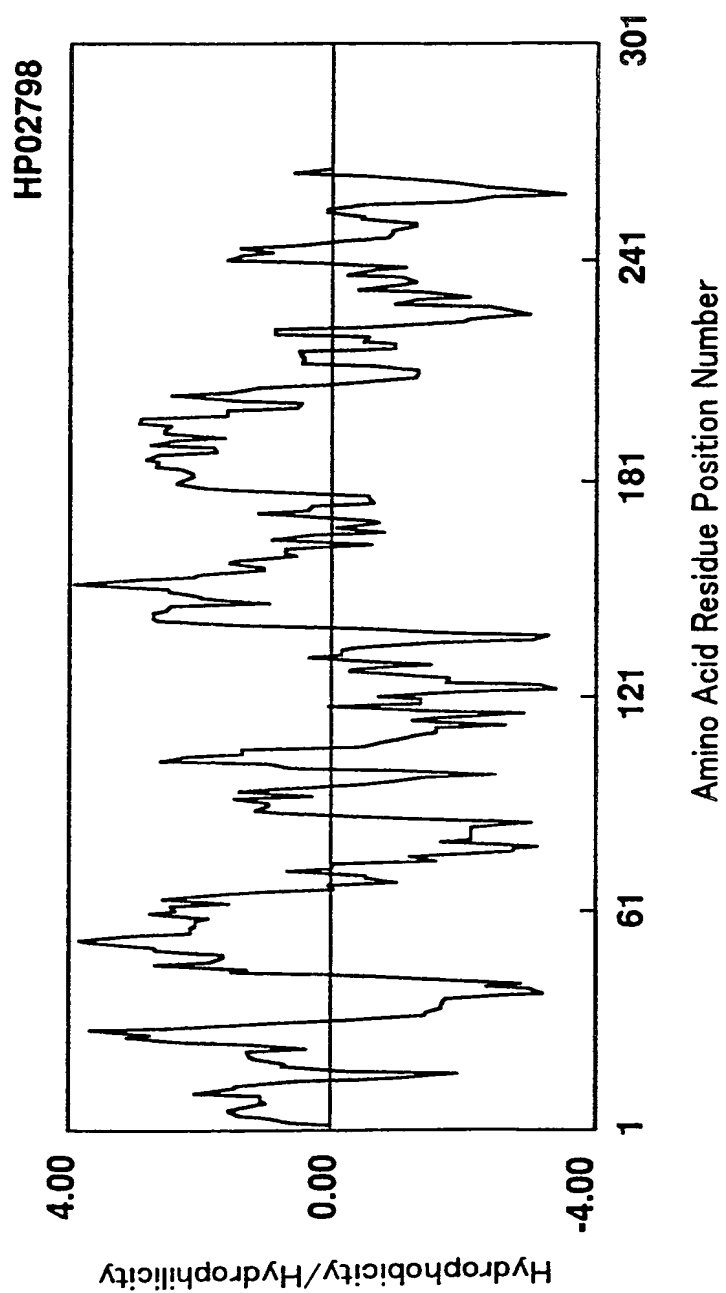


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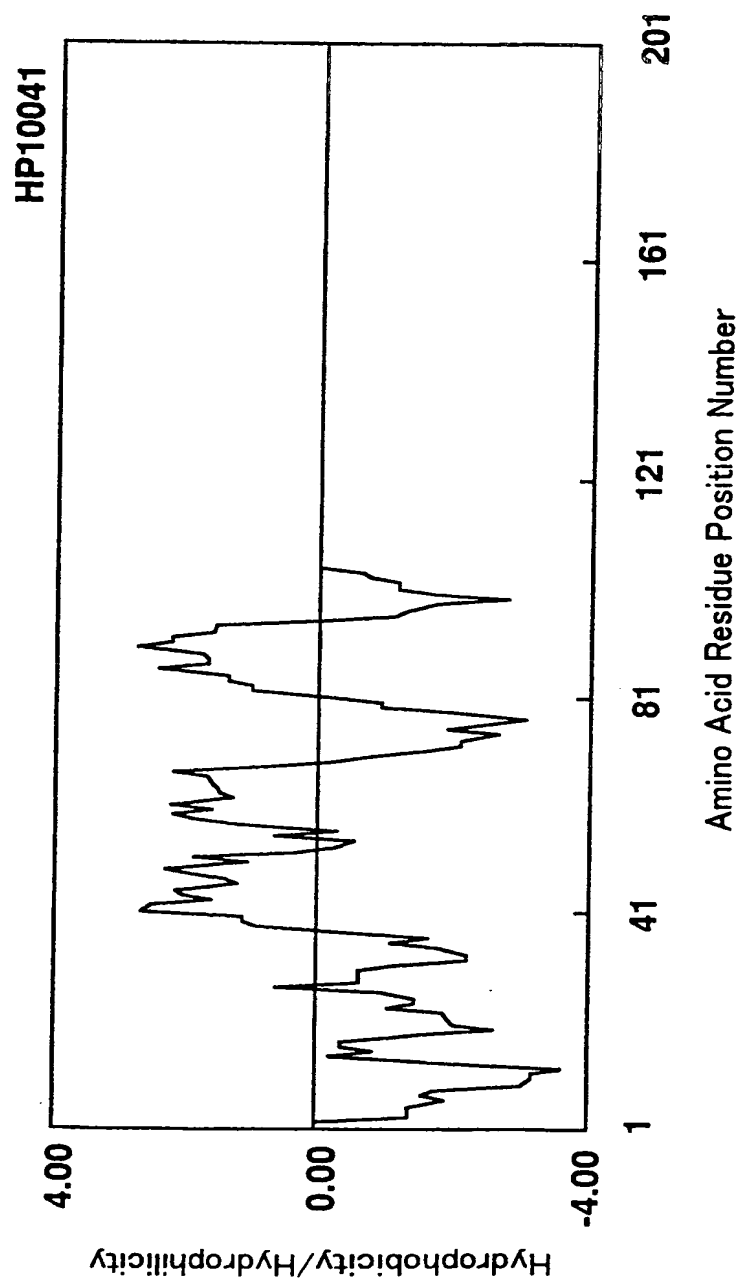


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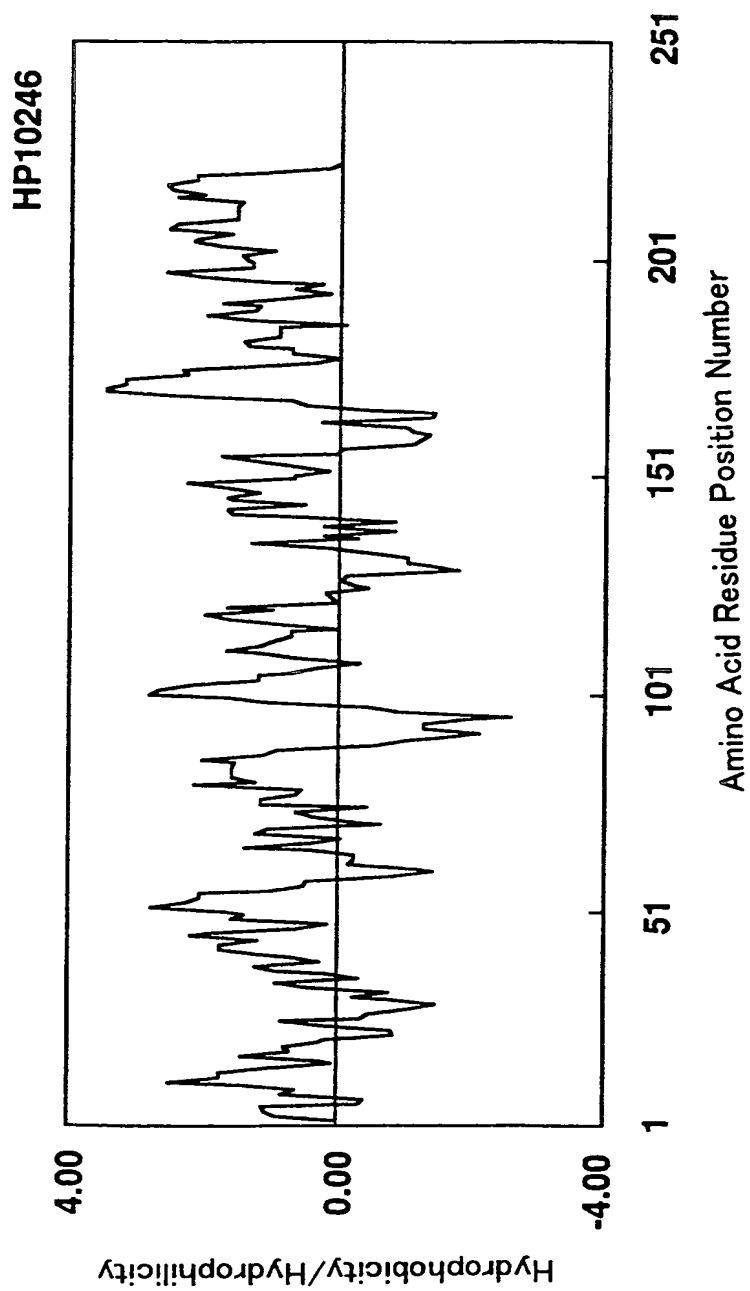


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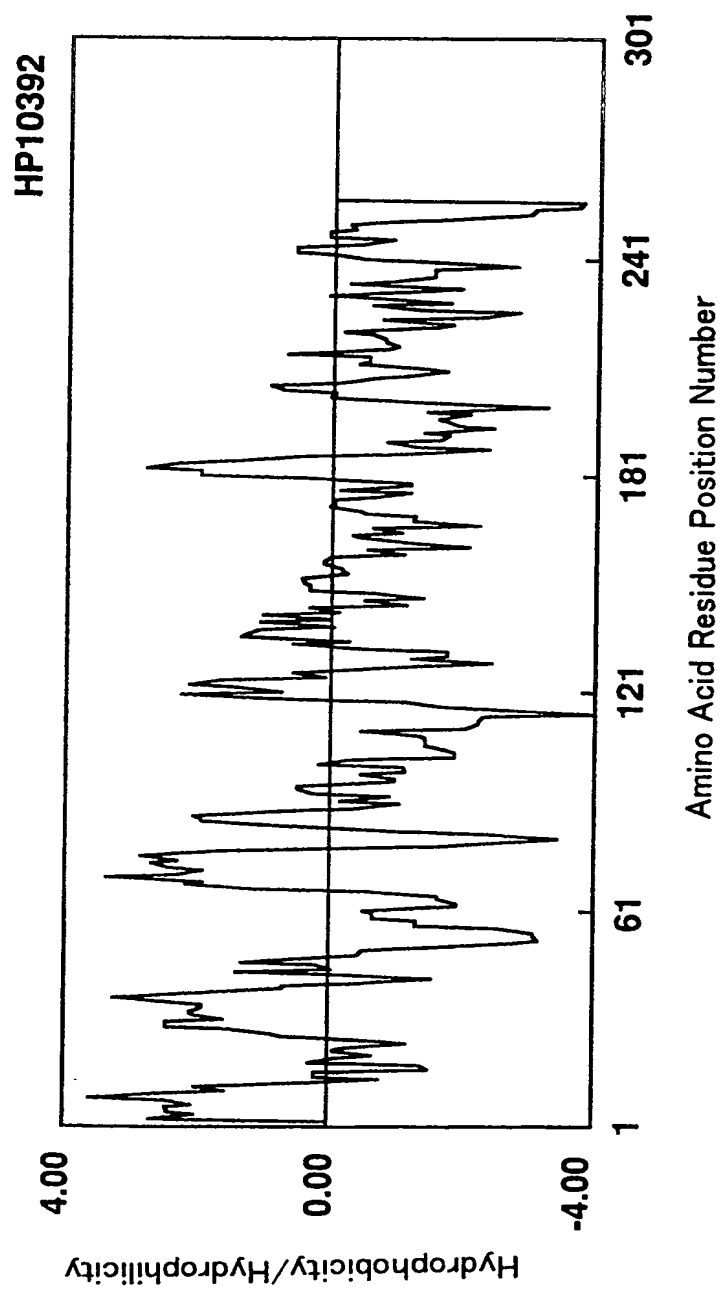


Fig. 46

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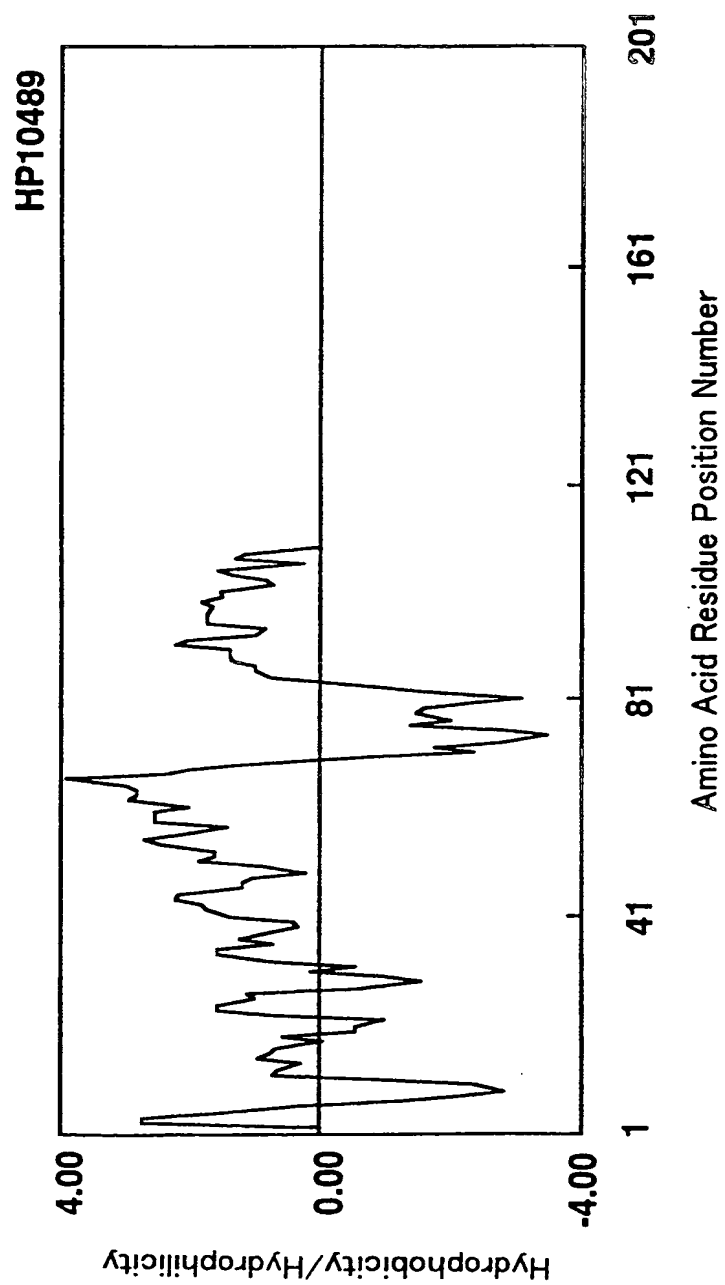


Fig.47

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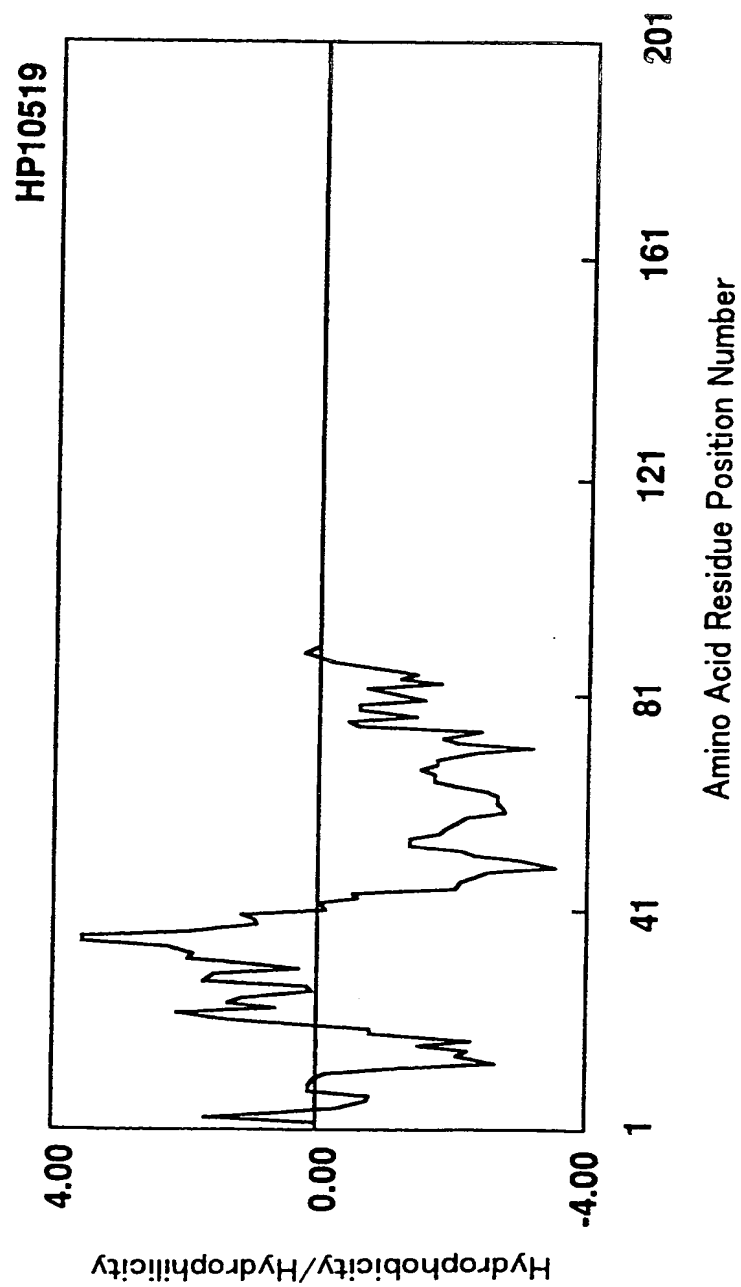


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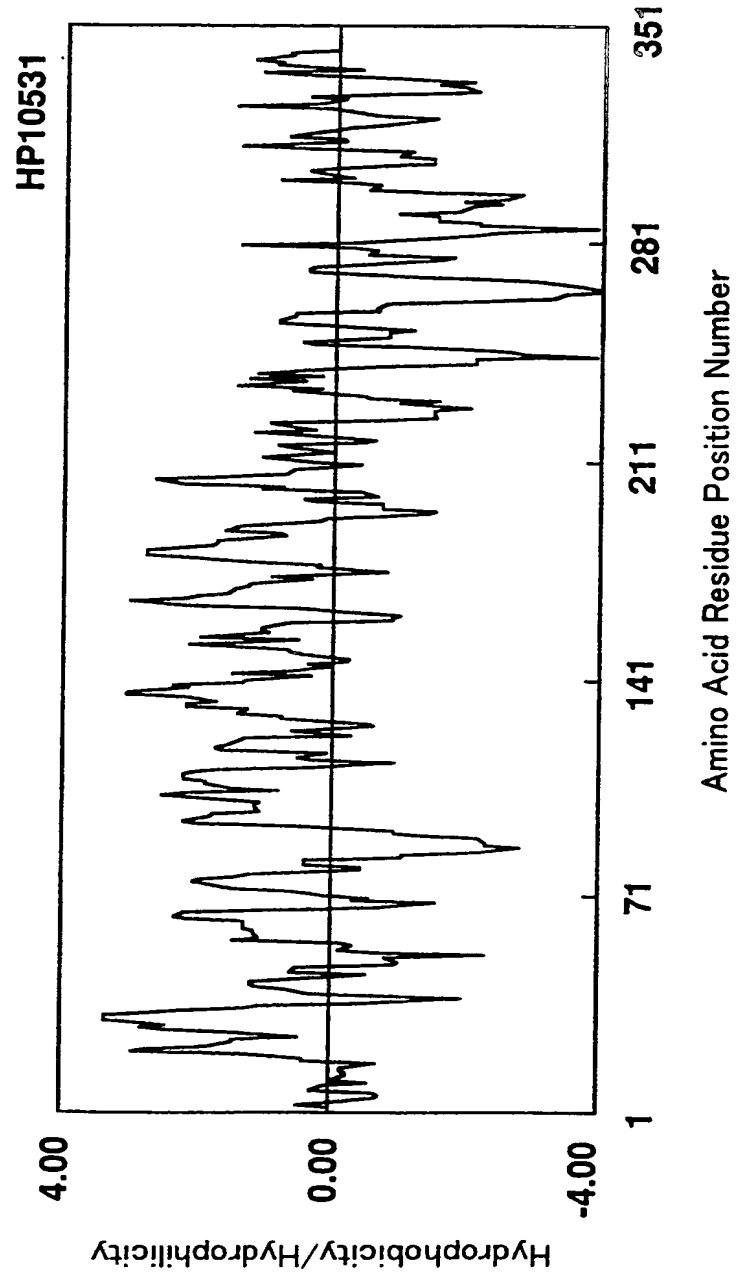


Fig. 49

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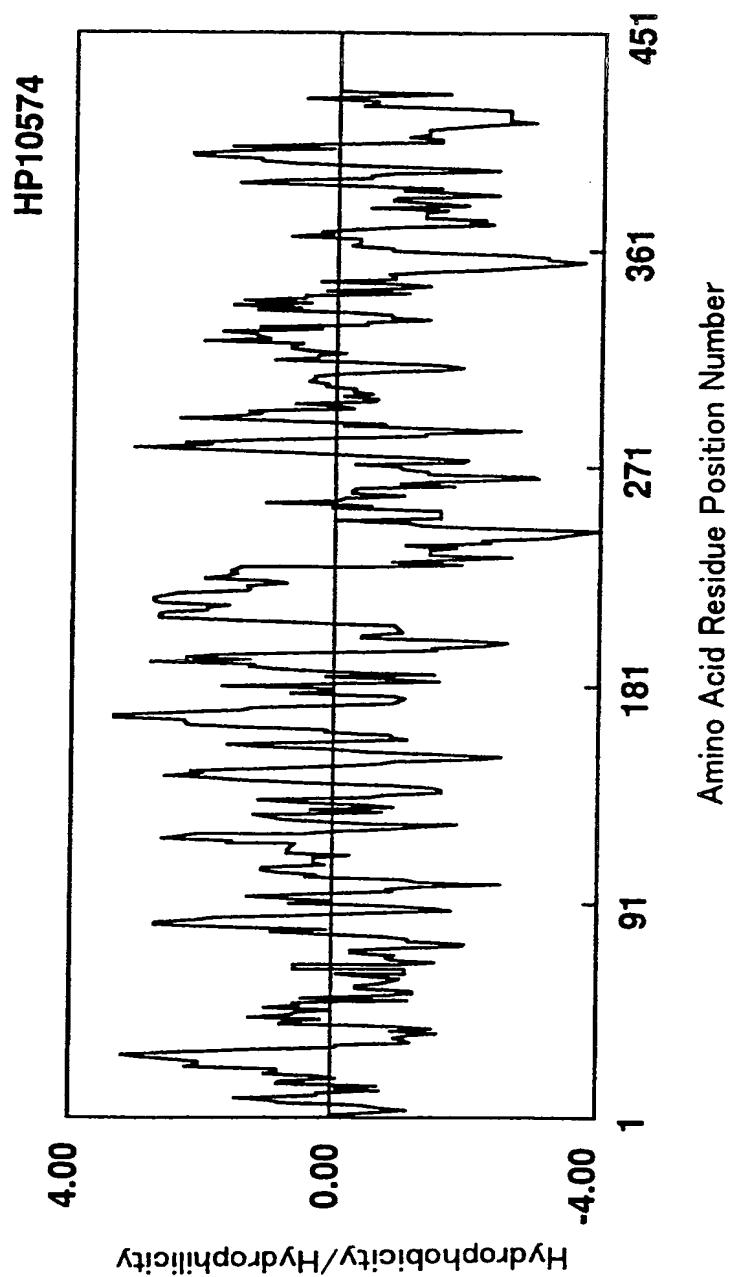


Fig. 50

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 15 Lys Phe Lys Gly Pro Phe Thr Asp Val Val Thr Thr Asn Leu Lys Leu
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 35 40 45
 Pro Arg Arg Tyr Cys Val Arg Pro Asn Ser Gly Ile Ile Asp Pro Gly
 20 50 55 60
 Ser Thr Val Thr Val Ser Val Met Leu Gln Pro Phe Asp Tyr Asp Pro
 65 70 75 80
 Asn Glu Lys Ser Lys His Lys Phe Met Val Gln Thr Ile Phe Ala Pro
 85 90 95
 25 Pro Asn Thr Ser Asp Met Glu Ala Val Trp Lys Glu Ala Lys Pro Asp
 100 105 110
 Glu Leu Met Asp Ser Lys Leu Arg Cys Val Phe Glu Met Pro Asn Glu
 115 120 125
 Asn Asp Lys Leu Asn Asp Met Glu Pro Ser Lys Ala Val Pro Leu Asn
 30 130 135 140
 Ala Ser Lys Gln Asp Gly Pro Met Pro Lys Pro His Ser Val Ser Leu
 145 150 155 160
 Asn Asp Thr Glu Thr Arg Lys Leu Met Glu Glu Cys Lys Arg Leu Gln
 165 170 175
 35 Gly Glu Met Met Lys Leu Ser Glu Glu Asn Arg His Leu Arg Asp Glu

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180 185 190
 Gly Leu Arg Leu Arg Lys Val Ala His Ser Asp Lys Pro Gly Ser Thr
 195 200 205
 Ser Thr Ala Ser Phe Arg Asp Asn Val Thr Ser Pro Leu Pro Ser Leu
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 Ile Leu

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 <212> PRT
 <213> Homo sapiens

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 35 40 45
 Thr Asp Cys Leu Val Pro Met Val Gly Asn Asn Pro Tyr Ala Thr Thr
 50 55 60
 Glu Gly Asn Ser Thr Glu Leu Ser Ile Asn Ala Glu Val Tyr Ser Leu
 25 65 70 75 80
 Pro Ser Arg Lys Leu Val Ala Leu Gln Leu Arg Ser Ile Phe Ile Lys
 85 90 95
 Tyr Lys Ser Lys Pro Phe Cys Glu Lys Leu Leu Ser Trp Val Lys Ser
 100 105 110
 30 Ser Gly Cys Ala Arg Val Ile Val Leu Ser Ser Ser His Ser Tyr Gln
 115 120 125
 Arg Asn Asp Leu Gln Leu Arg Ser Thr Pro Phe Arg Tyr Leu Leu Thr
 130 135 140
 Pro Ser Met Gln Lys Ser Val Gln Asn Lys Ile Lys Ser Leu Asn Trp
 35 145 150 155 160

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Glu Glu Met Glu Lys Ser Arg Cys Ile Pro Glu Ile Asp Asp Ser Glu
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 Phe Cys Ile Arg Ile Pro Gly Gly Gly Ile Thr Lys Thr Leu Tyr Asp
 180 185 190
 5 Glu Ser Cys Ser Lys Glu Ile Gln Met Ala Val Leu Leu Lys Phe Val
 195 200 205
 Ser Glu Gly Asp Asn Ile Pro Asp Ala Leu Gly Leu Val Glu Tyr Leu
 210 215 220
 Asn Glu Trp Leu Gln Ile Leu Lys Pro Leu Ser Asp Asp Pro Thr Val
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 Gly Ala Pro Thr Ser Pro Ala Glu His Arg Leu Leu Lys Thr Cys Trp
 35 40 45
 Ser Cys Arg Val Leu Ser Gly Leu Gly Leu Met Gly Ala Gly Gly Tyr
 50 55 60
 30 Val Tyr Trp Val Ala Arg Lys Pro Met Lys Met Gly Tyr Pro Pro Ser
 65 70 75 80
 Pro Trp Thr Ile Thr Gln Met Val Ile Gly Leu Ser Ile Ala Thr Trp
 85 90 95
 Gly Ile Val Val Met Ala Asp Pro Lys Gly Lys Ala Tyr Arg Val Val
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<211> 146

<212> PRT

5 <213> Homo sapiens

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Pro Val Gln Glu Glu Lys Leu Ser Ala Ser Thr Ser Asn Leu Pro Cys
35 40 45
Trp Leu Val Glu Glu Phe Val Val Ala Glu Glu Cys Ser Pro Cys Ser
15 50 55 60
Asn Phe Arg Ala Lys Thr Thr Pro Glu Cys Gly Pro Thr Gly Tyr Val
65 70 75 80
Glu Lys Ile Thr Cys Ser Ser Ser Lys Arg Asn Glu Phe Lys Ser Cys
85 90 95
20 Arg Ser Ala Leu Met Glu Gln Arg Leu Phe Trp Lys Phe Glu Gly Ala
100 105 110
Val Val Cys Val Ala Leu Ile Phe Ala Cys Leu Val Ile Ile Arg Gln
115 120 125
Arg Gln Leu Asp Arg Lys Ala Leu Glu Lys Val Arg Lys Gln Ile Glu
25 130 135 140
Ser Ile
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30 <211> 344

<212> PRT

<213> Homo sapiens

<400> 7

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		20		25		30										
	Leu	Ala	Arg	Gly	Gly	Ala	Gln	Ile	Phe	Ser	Cys	Ile	Ile	Pro	Glu	Cys
5		35		40		45										
	Leu	Gln	Arg	Ala	Val	His	Gly	Leu	Leu	His	Tyr	Leu	Phe	His	Thr	Arg
		50		55		60										
	Asn	His	Thr	Phe	Ile	Val	Leu	His	Leu	Val	Leu	Gln	Gly	Met	Val	Tyr
	65		70		75		80									
10	Thr	Glu	Tyr	Thr	Trp	Glu	Val	Phe	Gly	Tyr	Cys	Gln	Glu	Leu	Glu	Leu
		85		90		95										
	Ser	Leu	His	Tyr	Leu	Leu	Leu	Pro	Tyr	Leu	Leu	Leu	Gly	Val	Asn	Leu
		100		105		110										
	Phe	Phe	Phe	Thr	Leu	Thr	Cys	Gly	Thr	Asn	Pro	Gly	Ile	Ile	Thr	Lys
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	Ala	Asn	Glu	Leu	Leu	Phe	Leu	His	Val	Tyr	Glu	Phe	Asp	Glu	Val	Met
	130		135		140											
	Phe	Pro	Lys	Asn	Val	Arg	Cys	Ser	Thr	Cys	Asp	Leu	Arg	Lys	Pro	Ala
	145		150		155		160									
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		165		170		175										
	His	His	Cys	Val	Trp	Val	Asn	Asn	Cys	Ile	Gly	Ala	Trp	Asn	Ile	Arg
		180		185		190										
	Tyr	Phe	Leu	Ile	Tyr	Val	Leu	Thr	Leu	Thr	Ala	Ser	Ala	Ala	Thr	Val
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	225		230		235		240									
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		245		250		255										
	Val	Phe	Met	Leu	Gly	Phe	Val	Val	Val	Leu	Ser	Phe	Leu	Leu	Gly	Gly
		260		265		270										
	Tyr	Leu	Leu	Phe	Val	Leu	Tyr	Leu	Ala	Ala	Thr	Asn	Gln	Thr	Thr	Asn
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Glu Trp Tyr Arg Gly Asp Trp Ala Trp Cys Gln Arg Cys Pro Leu Val
 290 295 300
 Ala Trp Pro Pro Ser Ala Glu Pro Gln Val His Arg Asn Ile His Ser
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 Cys His Glu Arg Lys Lys Gln Glu
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 Leu Glu Lys Glu Lys Asn Ser Leu Met Asn Lys Ala Ser Asn Tyr Glu
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 Lys Glu Leu Lys Phe Leu Arg Gln Glu Asn Arg Lys Asn Met Leu Leu
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 5 Gly Lys Asn Glu Pro Glu Asp Ser Lys Leu Arg Phe Glu Thr Tyr Gln
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 50 55 60
 Leu Asn Lys Asn Leu Phe Asp Asn Leu Ile Glu Phe Leu Gln Lys Ser
 10 65 70 75 80
 His Ser Gly Phe Gln Lys Asn Ser Arg Asp Leu Gly Gly Gln Ile Lys
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 35 40 45
 30 Thr Ser Val Gly Asp Ser Phe Ala Leu Glu Trp Ser Phe Val Gln Pro
 50 55 60
 Gly Lys Pro Ile Ser Glu Ser His Pro Ile Leu Tyr Phe Thr Asn Gly
 65 70 75 80
 His Leu Tyr Pro Thr Gly Ser Lys Ser Lys Arg Val Ser Leu Leu Gln
 35 85 90 95

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 Pro Ser Asp Thr Gly Thr Tyr Leu Cys Gln Val Asn Asn Pro Pro Asp
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 5 Phe Tyr Thr Asn Gly Leu Gly Leu Ile Asn Leu Thr Val Leu Val Pro
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 Pro Ser Asn Pro Leu Cys Ser Gln Ser Gly Gln Thr Ser Val Gly Gly
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 Ser Thr Ala Leu Arg Cys Ser Ser Ser Glu Gly Ala Pro Lys Pro Val
 10 165 170 175
 Tyr Asn Trp Val Arg Leu Gly Thr Phe Pro Thr Pro Ser Pro Gly Ser
 180 185 190
 Met Val Gln Asp Glu Val Ser Gly Gln Leu Ile Leu Thr Asn Leu Ser
 195 200 205
 15 Leu Thr Ser Ser Gly Thr Tyr Arg Cys Val Ala Thr Asn Gln Met Gly
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 Ser Ala Ser Cys Glu Leu Thr Leu Ser Val Thr Glu Pro Ser Gln Gly
 225 230 235 240
 Arg Val Ala Gly Ala Leu Ile Gly Val Leu Leu Gly Val Leu Leu Leu
 20 245 250 255
 Ser Val Ala Ala Phe Cys Leu Val Arg Phe Gln Lys Glu Arg Gly Lys
 260 265 270
 Lys Pro Lys Glu Thr Tyr Gly Gly Ser Asp Leu Arg Glu Asp Ala Ile
 275 280 285
 25 Ala Pro Gly Ile Ser Glu His Thr Cys Met Arg Ala Asp Ser Ser Lys
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35 <213> Homo sapiens

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	cagattctca acgtgtccaa gctgagccct gaggaggtcc agaagaacta tgaacactta	240
	tttaaggtga atgataaatc cgtgggtggc tccttctacc tgcagtcaaa ggtggtccgc	300
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	cttgttctca caggaaacac agtcatcttt gcaactatac taggcttttt cttggtcttt	360
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	tgtttcaaag tgaagactac agcacctcgc cggtagctg tgaggcccaa cagtggaatt	180
	attgacctag ggtcaactgt gactgtttca gtaatgctac agccctttga ctatgatccg	240
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	tgcgtatttg aaatgccc aa tgaaaatgat aaattgaatg atatggaacc tagcaaagct	420
	gttccactga atgcatctaa gcaagatgga cctatgccaa aaccacacag tgtttcactt	480
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	atggcagttc tgctgaaatt tgtttcagaa ggggacaaca tcccagatgc attaggtctt	660
	gttgagtatc ttaatgagtg gcttcagata ctcaaacaccac ttagcgatga ccccacagta	720
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 caccgcctgt tgaagacctg ctggagctgt cgcgtgcttt ctgggttggg gctgatgggg 180
 5 gggggcgggt acgtgtactg ggtggcacgg aagcccatga agatgggata cccccgagt 240
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<212> DNA

<213> Homo sapiens

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 gcttgtcttg tcatcattcg tcagcgacaa ttggacagaa aggtcttgga aaaggtccgg 420
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	tccaactacg agaaggaact gaagtttctt cggcaagaga accggaagaa catgctgctc	240
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	aagcttcgat tcgaaactta tcagttgata tggcagcaga tgaaatctga aaatgagcga	180
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Met Ala Lys Tyr Leu Ala Gln Ile Ile Val Met Gly Val Gln Val

1

5

10

15

gtg gcc agg gcc ttt gca cgg gcc ttg cgg cag gag ttt gca gcc agc 158
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40

45

gct tcc aac ctc tcc ggc ctc agc ctc cag gag gca cag cag att ctc 254
 Ala Ser Asn Leu Ser Gly Leu Ser Leu Gln Glu Ala Gln Gln Ile Leu

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50

55

60

aac gtg tcc aag ctg agc cct gag gag gtc cag aag aac tat gaa cac 302
 Asn Val Ser Lys Leu Ser Pro Glu Glu Val Gln Lys Asn Tyr Glu His

65

70

75

20

tta ttt aag gtg aat gat aaa tcc gtg ggt ggc tcc ttc tac ctg cag 350
 Leu Phe Lys Val Asn Asp Lys Ser Val Gly Gly Ser Phe Tyr Leu Gln

80

85

90

95

tca aag gtg gtc cgc gca aag gag cgc ctg gat gag gaa ctc aaa atc 398
 Ser Lys Val Val Arg Ala Lys Glu Arg Leu Asp Glu Glu Leu Lys Ile

100

105

110

25

cag gcc cag gag gac aga gaa aaa ggg cag atg ccc cat acg tgactgctc 450
 Gln Ala Gln Glu Asp Arg Glu Lys Gly Gln Met Pro His Thr

115

120

125

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5	cgccg	ccgcc	tcggg	tcgtg	gagcc	aggag	cgacg	tcacc	gcc	atg	gca	ggc	115
	Met Ala Gly Ile												
	1												
	aaa	gct	ttg	att	agt	ttg	tcc	ttt	gga	gga	gca	atc	163
	Lys	Ala	Leu	Ile	Ser	Leu	Ser	Phe	Gly	Gly	Ala	Ile	
10	5		10			15			20				
	ttg	atg	ctt	gga	tgt	gcc	ctt	cca	ata	tac	aac	aaa	211
	Leu	Met	Leu	Gly	Cys	Ala	Leu	Pro	Ile	Tyr	Asn	Lys	
	25 30 35												
	ttt	ggt	cta	ttt	ttt	tac	atc	ctt	tca	cct	att	cca	259
15	Phe	Val	Leu	Phe	Phe	Tyr	Ile	Leu	Ser	Pro	Ile	Pro	
	40 45 50												
	aga	aga	tta	gtg	gat	gat	aca	gat	gct	atg	agt	aac	307
	Arg	Arg	Leu	Val	Asp	Asp	Thr	Asp	Ala	Met	Ser	Asn	
	55 60 65												
20	ctt	gcc	atc	ttt	ctt	aca	acg	ggc	att	gtc	gtg	tca	355
	Leu	Ala	Ile	Phe	Leu	Thr	Thr	Gly	Ile	Val	Val	Ser	
	70 75 80												
	cct	att	gta	ttt	gcc	aga	gca	cat	ctg	att	gag	tggt	403
	Pro	Ile	Val	Phe	Ala	Arg	Ala	His	Leu	Ile	Glu	Trp	
25	85		90			95			100				
	ctt	gtt	ctc	aca	gga	aac	aca	gtc	atc	ttt	gca	act	451
	Leu	Val	Leu	Thr	Gly	Asn	Thr	Val	Ile	Phe	Ala	Thr	
	105 110 115												
	ttc	ttg	gtc	ttt	gga	agc	aat	gac	gac	ttc	agc	tggt	500
30	Phe	Leu	Val	Phe	Gly	Ser	Asn	Asp	Asp	Phe	Ser	Trp	
	120 125 130												
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	caggag	atgg	ggcag	ttaat	gtg	aatgg	atagc	aagcc	tcttg	ggggg	at	tttag	620
	ctccct	tctc	actttt	tattg	taagc	atact	at	tttcacag	agact	tgtg	aaggat	taaa	680
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 gtgacacagc ggcaggcgtt agggctcggg agccgcgagc ctggcctcgt cctagagctc 180
 ggccgagcgc tcgccgccgt cgtcccccgc cccagtcag caaaccgccg ccgcggggcgc 240
 15 gcccccgctc tgcgctgtct ctccgatggc gtccgcctca ggggcc atg gcg aag 295
 Met Ala Lys
 1
 cac gag cag atc ctg gtc ctc gat ccg ccc aca gac ctc aaa ttc aaa 343
 His Glu Gln Ile Leu Val Leu Asp Pro Pro Thr Asp Leu Lys Phe Lys
 20 5 10 15
 ggc ccc ttc aca gat gta gtc act aca aat ctt aaa ttg cga aat cca 391
 Gly Pro Phe Thr Asp Val Val Thr Thr Asn Leu Lys Leu Arg Asn Pro
 20 25 30 35
 tcg gat aga aaa gtg tgt ttc aaa gtg aag act aca gca cct cgc cgg 439
 25 Ser Asp Arg Lys Val Cys Phe Lys Val Lys Thr Thr Ala Pro Arg Arg
 40 45 50
 tac tgt gtg agg ccc aac agt gga att att gac cca ggg tca act gtg 487
 Tyr Cys Val Arg Pro Asn Ser Gly Ile Ile Asp Pro Gly Ser Thr Val
 55 60 65
 30 act gtt tca gta atg cta cag ccc ttt gac tat gat ccg aat gaa aag 535
 Thr Val Ser Val Met Leu Gln Pro Phe Asp Tyr Asp Pro Asn Glu Lys
 70 75 80
 agt aaa cac aag ttt atg gta cag aca att ttt gct cca cca aac act 583
 Ser Lys His Lys Phe Met Val Gln Thr Ile Phe Ala Pro Pro Asn Thr
 35 85 90 95

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	Ser Asp Met Glu Ala Val Trp Lys Glu Ala Lys Pro Asp Glu Leu Met	
	100 105 110 115	
	gat tcc aaa ttg aga tgc gta ttt gaa atg ccc aat gaa aat gat aaa	679
5	Asp Ser Lys Leu Arg Cys Val Phe Glu Met Pro Asn Glu Asn Asp Lys	
	120 125 130	
	ttg aat gat atg gaa cct agc aaa gct gtt cca ctg aat gca tct aag	727
	Leu Asn Asp Met Glu Pro Ser Lys Ala Val Pro Leu Asn Ala Ser Lys	
	135 140 145	
10	caa gat gga cct atg cca aaa cca cac agt gtt tca ctt aat gat acc	775
	Gln Asp Gly Pro Met Pro Lys Pro His Ser Val Ser Leu Asn Asp Thr	
	150 155 160	
	gaa aca agg aaa cta atg gaa gag tgt aaa aga ctt cag gga gaa atg	823
	Glu Thr Arg Lys Leu Met Glu Glu Cys Lys Arg Leu Gln Gly Glu Met	
15	165 170 175	
	atg aag cta tca gaa gaa aat cgg cac ctg aga gat gaa ggt tta agg	871
	Met Lys Leu Ser Glu Glu Asn Arg His Leu Arg Asp Glu Gly Leu Arg	
	180 185 190 195	
	ctc aga aag gta gca cat tcg gat aaa cct gga tca acc tca act gca	919
20	Leu Arg Lys Val Ala His Ser Asp Lys Pro Gly Ser Thr Ser Thr Ala	
	200 205 210	
	tcc ttc aga gat aat gtc acc agt cct ctt cct tca ctt ctt gtt gta	967
	Ser Phe Arg Asp Asn Val Thr Ser Pro Leu Pro Ser Leu Leu Val Val	
	215 220 225	
25	att gca gcc att ttc att gga ttc ttt cta ggg aaa ttc atc ttg	1012
	Ile Ala Ala Ile Phe Ile Gly Phe Phe Leu Gly Lys Phe Ile Leu	
	230 235 240	
	tagagtgaag catgcagagt gctgtttcct tttttttttt ttctcttgac cagaaaaa	1070
	gatttggtta cctaccattt catttgtagt atggcccacg gtgaccattt ttttggtgtg	1130
30	acagcgtcat ataggctttg cctttaatga tctcttacgg ttagaaaaca caataaaaac	1190
	aaactgttcg gctactggac aggttgata ttaccagatc atcactagca gatgtcagtt	1250
	gcacattgag tcctttatga aattcataaa taaagaattg ttctttcttt gtggttttaa	1310
	taagagtcca agaattgttc agagtcttgt aaatgttatt ttaataatcc ctttaaattt	1370
	tatctgttgc tgttacctct tgaaatatga tttatttaga ttgctaatacc cactcattea	1430
35	ggaaatgcca agaggtattc cttggggaaa tgggtgcctct tacagtgtaa atttttctc	1490

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 Met Phe Val Pro Cys Gly Glu Ser Ala Pro Asp Leu Ala Gly Phe
 1 5 10 15
 acc ctc cta atg cca gca gta tct gtt gga aat gtt ggc cag ctt gca 157
 Thr Leu Leu Met Pro Ala Val Ser Val Gly Asn Val Gly Gln Leu Ala
 20 20 25 30
 atg gat ctg att att tct aca ctg aat atg tct aag att ggt tac ttc 205
 Met Asp Leu Ile Ile Ser Thr Leu Asn Met Ser Lys Ile Gly Tyr Phe
 35 40 45
 tat acc gat tgt ctt gtg cca atg gtt gga aac aat cca tat gcg acc 253
 25 Tyr Thr Asp Cys Leu Val Pro Met Val Gly Asn Asn Pro Tyr Ala Thr
 50 55 60
 aca gaa gga aat tca aca gaa ctt agc ata aat gct gaa gtg tat tca 301
 Thr Glu Gly Asn Ser Thr Glu Leu Ser Ile Asn Ala Glu Val Tyr Ser
 65 70 75
 ttg cct tca aga aag ctg gtg gct cta cag tta aga tcc att ttt att 349
 30 Leu Pro Ser Arg Lys Leu Val Ala Leu Gln Leu Arg Ser Ile Phe Ile
 80 85 90 95
 aag tat aaa tca aag cca ttc tgt gaa aaa ctg ctt tcc tgg gtg aaa 397
 Lys Tyr Lys Ser Lys Pro Phe Cys Glu Lys Leu Leu Ser Trp Val Lys
 35 100 105 110

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agc agt ggc tgt gcc aga gtc att gtt ctt tcg agc agt cat tca tat 445
 Ser Ser Gly Cys Ala Arg Val Ile Val Leu Ser Ser Ser His Ser Tyr
 115 120 125
 5 cag cgt aat gat ctg cag ctt cgt agt act ccc ttc cgg tac cta ctt 493
 Gln Arg Asn Asp Leu Gln Leu Arg Ser Thr Pro Phe Arg Tyr Leu Leu
 130 135 140
 aca cct tcc atg caa aaa agt gtt caa aat aaa ata aag agc ctt aac 541
 Thr Pro Ser Met Gln Lys Ser Val Gln Asn Lys Ile Lys Ser Leu Asn
 145 150 155
 10 tgg gaa gaa atg gaa aaa agc cgg tgc att cct gaa ata gat gat tcc 589
 Trp Glu Glu Met Glu Lys Ser Arg Cys Ile Pro Glu Ile Asp Asp Ser
 160 165 170 175
 gag ttt tgt atc cgc att ccg gga gga ggt atc aca aaa aca ctc tat 637
 Glu Phe Cys Ile Arg Ile Pro Gly Gly Gly Ile Thr Lys Thr Leu Tyr
 15 180 185 190
 gat gaa agc tgt tct aaa gaa atc caa atg gca gtt ctg ctg aaa ttt 685
 Asp Glu Ser Cys Ser Lys Glu Ile Gln Met Ala Val Leu Leu Lys Phe
 195 200 205
 gtt tca gaa ggg gac aac atc cca gat gca tta ggt ctt gtt gag tat 733
 20 Val Ser Glu Gly Asp Asn Ile Pro Asp Ala Leu Gly Leu Val Glu Tyr
 210 215 220
 ctt aat gag tgg ctt cag ata ctc aaa cca ctt agc gat gac ccc aca 781
 Leu Asn Glu Trp Leu Gln Ile Leu Lys Pro Leu Ser Asp Asp Pro Thr
 225 230 235
 25 gta tct gcc tca cgg tgg aaa ata cca agt tct tgg aga tta ctc ttt 829
 Val Ser Ala Ser Arg Trp Lys Ile Pro Ser Ser Trp Arg Leu Leu Phe
 240 245 250 255
 ggc agt ggt ctt ccc cct gca ctt ttc tgatctaatt tctgttttat acct 880
 Gly Ser Gly Leu Pro Pro Ala Leu Phe
 30 260
 tatacccaaaa acacttacta ccaacacagc tggttaaacad tctatacaaaa aaaattgtat 940
 gatctggtat taggaaatta ctttcacagt aaatatcaaaa gaaaaaagat taaggggtctc 1000
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<211> 618

<212> DNA

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	Gly Ser Arg Leu Ser Gln Pro Phe Glu Ser Tyr Ile Thr Ala Pro Pro	
15	5 10 15	
	ggt acc gcc gcc gcg ccc gcc aaa cct gcg ccc cca gct aca ccc gga	152
	Gly Thr Ala Ala Ala Pro Ala Lys Pro Ala Pro Pro Ala Thr Pro Gly	
	20 25 30	
	gcg ccg acc tcc cca gca gaa cac cgc ctg ttg aag acc tgc tgg agc	200
20	Ala Pro Thr Ser Pro Ala Glu His Arg Leu Leu Lys Thr Cys Trp Ser	
	35 40 45	
	tgt cgc gtg ctt tct ggg ttg ggg ctg atg ggg gcg ggc ggg tac gtg	248
	Cys Arg Val Leu Ser Gly Leu Gly Leu Met Gly Ala Gly Gly Tyr Val	
	50 55 60 65	
25	tac tgg gtg gca cgg aag ccc atg aag atg gga tac ccc ccg agt cca	296
	Tyr Trp Val Ala Arg Lys Pro Met Lys Met Gly Tyr Pro Pro Ser Pro	
	70 75 80	
	tgg acc att acg cag atg gtc atc ggc ctc agc att gcc acc tgg ggt	344
	Trp Thr Ile Thr Gln Met Val Ile Gly Leu Ser Ile Ala Thr Trp Gly	
30	85 90 95	
	atc gtt gtc atg gca gac ccc aaa ggg aag gcc tac cgc gtt gtt t	390
	Ile Val Val Met Ala Asp Pro Lys Gly Lys Ala Tyr Arg Val Val	
	100 105 110	
	gaaagtacca ccagtgaatc tgtcttctgt ctctgtccct ttccccgtga cacacacagc	450
35	aggcatggaa tttaatgggt gttctggaca gacacttgta catggacaga catcactact	510

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15 ggtgagcggg cgctagggcc gcgagccccg gccggccctt cctccagcgc cctgcggacc 180
ccgcagaagg cgctcgctc cctagccgcg aaaaacatat cgatttttct cgctgtggca 240
acggggacgt cctgatagat cctctgctcc aataggcaac tccggccttc cctgccctga 300
cctggaacct ctgggagggc tgcagagtaa gtgccgcctc tgcgctccga cggaggcacg 360
aggcctgtgg agtaggtccc tctgttccga caggtgcgac acttggeget cc atg ctt 418
20                                     Met Leu
                                     1

gcg ggt gcc ggg agg cct ggc ctc ccc cag ggc cgc cac ctc tgc tgg 466
Ala Gly Ala Gly Arg Pro Gly Leu Pro Gln Gly Arg His Leu Cys Trp
      5              10              15

25 ttg ctc tgt gct ttc acc tta aag ctc tgc caa gca gag gct ccc gtg 514
Leu Leu Cys Ala Phe Thr Leu Lys Leu Cys Gln Ala Glu Ala Pro Val
      20              25              30

cag gaa gag aag ctg tca gca agc acc tca aat ttg cca tgc tgg ctg 562
Gln Glu Glu Lys Leu Ser Ala Ser Thr Ser Asn Leu Pro Cys Trp Leu
30 35              40              45              50

gtg gaa gag ttt gtg gta gca gaa gag tgc tct cca tgc tct aat ttc 610
Val Glu Glu Phe Val Val Ala Glu Glu Cys Ser Pro Cys Ser Asn Phe
      55              60              65

cgg gct aaa act acc cct gag tgt ggt ccc aca gga tat gta gag aaa 658
35 Arg Ala Lys Thr Thr Pro Glu Cys Gly Pro Thr Gly Tyr Val Glu Lys

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	Ile Thr Cys Ser Ser Ser Lys Arg Asn Glu Phe Lys Ser Cys Arg Ser			
	85	90	95	
5	gct ttg atg gaa caa cgc tta ttt tgg aag ttc gaa ggg gct gtc gtg			754
	Ala Leu Met Glu Gln Arg Leu Phe Trp Lys Phe Glu Gly Ala Val Val			
	100	105	110	
	tgt gtg gcc ctg atc ttc gct tgt ctt gtc atc att cgt cag cga caa			802
	Cys Val Ala Leu Ile Phe Ala Cys Leu Val Ile Ile Arg Gln Arg Gln			
10	115	120	125	130
	ttg gac aga aag gct ctg gaa aag gtc cgg aag caa atc gag tcc ata			850
	Leu Asp Arg Lys Ala Leu Glu Lys Val Arg Lys Gln Ile Glu Ser Ile			
	135	140	145	
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15	aaatggactg atttgcactc ttggttcttt ggagccttgt ggtggaatcc ccttttcccc			970
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	ccagggtcc agccccagc gaaatctccg accaggcccg ccaggagcc agatccaggc			180
30	tcttgaaga accatgtccg gcagctactg gtcattgccag gcacacactg ctgcccaaga			240
	ggagctgctg tttgaattat ctgtgaatgt tgggaagagg aatgccagag ctgccggctg			300
	aaaattaccc aaccaagaga aatctgcagg atg gac ttt ctg gtc ctc ttc ttg			354
	Met Asp Phe Leu Val Leu Phe Leu			
	1	5		
35	ttc tac ctg gct tcg gtg ctg atg ggt ctt gtt ctt atc tgc gtc tgc			402

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	Phe Tyr Leu Ala Ser Val Leu Met Gly Leu Val Leu Ile Cys Val Cys	
	10 15 20	
	tcg aaa acc cat agc ttg aaa ggc ctg gcc agg gga gga gca cag ata	450
	Ser Lys Thr His Ser Leu Lys Gly Leu Ala Arg Gly Gly Ala Gln Ile	
5	25 30 35 40	
	ttt tcc tgt ata att cca gaa tgt ctt cag aga gcc gtg cat gga ttg	498
	Phe Ser Cys Ile Ile Pro Glu Cys Leu Gln Arg Ala Val His Gly Leu	
	45 50 55	
	ctt cat tac ctt ttc cat acg aga aac cac acc ttc att gtc ctg cac	546
10	Leu His Tyr Leu Phe His Thr Arg Asn His Thr Phe Ile Val Leu His	
	60 65 70	
	ctg gtc ttg caa ggg atg gtt tat act gag tac acc tgg gaa gta ttt	594
	Leu Val Leu Gln Gly Met Val Tyr Thr Glu Tyr Thr Trp Glu Val Phe	
	75 80 85	
15	ggc tac tgt cag gag ctg gag ttg tcc ttg cat tac ctt ctt ctg ccc	642
	Gly Tyr Cys Gln Glu Leu Glu Leu Ser Leu His Tyr Leu Leu Leu Pro	
	90 95 100	
	tat ctg ctg cta ggt gta aac ctg ttt ttt ttc acc ctg act tgt gga	690
	Tyr Leu Leu Leu Gly Val Asn Leu Phe Phe Phe Thr Leu Thr Cys Gly	
20	105 110 115 120	
	acc aat cct ggc att ata aca aaa gca aat gaa tta tta ttt ctt cat	738
	Thr Asn Pro Gly Ile Ile Thr Lys Ala Asn Glu Leu Leu Phe Leu His	
	125 130 135	
	gtt tat gaa ttt gat gaa gtg atg ttt cca aag aac gtg agg tgc tct	786
25	Val Tyr Glu Phe Asp Glu Val Met Phe Pro Lys Asn Val Arg Cys Ser	
	140 145 150	
	act tgt gat tta agg aaa cca gct cga tcc aag cac tgc agt gtg tgt	834
	Thr Cys Asp Leu Arg Lys Pro Ala Arg Ser Lys His Cys Ser Val Cys	
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30	aac tgg tgt gtg cac cgt ttc gac cat cac tgt gtt tgg gtg aac aac	882
	Asn Trp Cys Val His Arg Phe Asp His His Cys Val Trp Val Asn Asn	
	170 175 180	
	tgc atc ggg gcc tgg aac atc agg tac ttc ctc atc tac gtc ttg acc	930
	Cys Ile Gly Ala Trp Asn Ile Arg Tyr Phe Leu Ile Tyr Val Leu Thr	
35	185 190 195 200	

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5	gtc cac ttg gtg gtg atg tca gat tta tac cag gag act tac atc gat	1026
	Val His Leu Val Val Met Ser Asp Leu Tyr Gln Glu Thr Tyr Ile Asp	
	220 225 230	
	gac ctt gga cac ctc cat gtt atg gac acg gtc ttt ctt att cag tac	1074
	Asp Leu Gly His Leu His Val Met Asp Thr Val Phe Leu Ile Gln Tyr	
	235 240 245	
10	ctg ttc ctg act ttt cca cgg att gtc ttc atg ctg ggc ttt gtc gtg	1122
	Leu Phe Leu Thr Phe Pro Arg Ile Val Phe Met Leu Gly Phe Val Val	
	250 255 260	
	GTT CTG AGC TTC CTC CTG GGT GGC TAC CTG TTG TTT GTC CTG TAT CTG	1170
	Val Leu Ser Phe Leu Leu Gly Gly Tyr Leu Leu Phe Val Leu Tyr Leu	
15	265 270 275 280	
	gcg gcc acc aac cag act act aac gag tgg tac aga ggt gac tgg gcc	1218
	Ala Ala Thr Asn Gln Thr Thr Asn Glu Trp Tyr Arg Gly Asp Trp Ala	
	285 290 295	
20	tgg tgc cag cgt tgt ccc ctt gtg gcc tgg cct ccg tca gca gag ccc	1266
	Trp Cys Gln Arg Cys Pro Leu Val Ala Trp Pro Pro Ser Ala Glu Pro	
	300 305 310	
	caa gtc cac cgg aac att cac tcc cat ggg ctt cgg agc aac ctt caa	1314
	Gln Val His Arg Asn Ile His Ser His Gly Leu Arg Ser Asn Leu Gln	
	315 320 325	
25	gag atc ttt cta cct gcc ttt cca tgt cat gag agg aag aaa caa gaa	1362
	Glu Ile Phe Leu Pro Ala Phe Pro Cys His Glu Arg Lys Lys Gln Glu	
	330 335 340	
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	tcgttttcca ag	1432
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	Met Thr Lys Lys Lys Arg Glu Asn Leu Gly Val Ala Leu Glu Ile Asp	
	1 5 10 15	
	ggg cta gag gag aag ctg tcc cag tgt cgg aga gac ctg gag gcc gtg	157
10	Gly Leu Glu Glu Lys Leu Ser Gln Cys Arg Arg Asp Leu Glu Ala Val	
	20 25 30	
	aac tcc aga ctc cac agc cgg gag ctg agc cca gag gcc agg agg tcc	205
	Asn Ser Arg Leu His Ser Arg Glu Leu Ser Pro Glu Ala Arg Arg Ser	
	35 40 45	
15	ctg gag aag gag aaa aac agc cta atg aac aaa gcc tcc aac tac gag	253
	Leu Glu Lys Glu Lys Asn Ser Leu Met Asn Lys Ala Ser Asn Tyr Glu	
	50 55 60	
	aag gaa ctg aag ttt ctt cgg caa gag aac cgg aag aac atg ctg ctc	301
	Lys Glu Leu Lys Phe Leu Arg Gln Glu Asn Arg Lys Asn Met Leu Leu	
20	65 70 75 80	
	tct gtg gcc atc ttt atc ctc ctg acg ctc gtc tat gcc tac tgg acc	349
	Ser Val Ala Ile Phe Ile Leu Leu Thr Leu Val Tyr Ala Tyr Trp Thr	
	85 90 95	
	atg tgagcctggc acttccccac aaccagcaca ggcttccact tggcccct	400
25	Met	
	tgatcaggat caagcaggca cttcaagcct caataggacc aaggtgctgg ggtgttcccc	460
	tcccaacctt gtgttcaagc atggetteet ggcgccccag gccttgccct cctggcctgc	520
	tgggggggttc cgggtctcca gaaggacatg gtgctgtgcc ctcccttagc ccaagggaga	580
30	ggcaataaag acacaaagct g	601

<210> 29

<211> 585

<212> DNA

35 <213> Homo sapiens

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<220>

<221> CDS

<222> (78)...(452)

5 <400> 29

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gcagagtcag taagacc atg gct acg tcc tcg atg tct aag ggt tgc ttt 110

Met Ala Thr Ser Ser Met Ser Lys Gly Cys Phe

1 5 10

10 gtt ttt aag cca aac tcc aaa aag aga aag atc tct ctg cca ata gag 158

Val Phe Lys Pro Asn Ser Lys Lys Arg Lys Ile Ser Leu Pro Ile Glu

15 20 25

gac tat ttt aac aaa ggg aaa aat gag cct gag gac agt aag ctt cga 206

Asp Tyr Phe Asn Lys Gly Lys Asn Glu Pro Glu Asp Ser Lys Leu Arg

15 30 35 40

ttc gaa act tat cag ttg ata tgg cag cag atg aaa tct gaa aat gag 254

Phe Glu Thr Tyr Gln Leu Ile Trp Gln Gln Met Lys Ser Glu Asn Glu

45 50 55

cga cta caa gag gaa tta aat aaa aac ttg ttt gac aat ctg att gaa 302

20 Arg Leu Gln Glu Glu Leu Asn Lys Asn Leu Phe Asp Asn Leu Ile Glu

60 65 70 75

ttt ctg caa aaa tca cat tct gga ttc cag aag aat tca aga gac ttg 350

Phe Leu Gln Lys Ser His Ser Gly Phe Gln Lys Asn Ser Arg Asp Leu

80 85 90

25 ggc ggt caa ata aaa ctc aga gaa att cca act gct gct ctt gtt ctt 398

Gly Gly Gln Ile Lys Leu Arg Glu Ile Pro Thr Ala Ala Leu Val Leu

95 100 105

ggt ata tat gcg tat gtt tgt tca tgc atg cat ctc tgt gta ttt cgt 446

Gly Ile Tyr Ala Tyr Val Cys Ser Cys Met His Leu Cys Val Phe Arg

110 115 120

30 ttt taaat tttttt tttattgttg agaatagtgg aaggacctgt tttgatgagc c 500

Phe

tattttgtct ctcttatttg tacaattaaa ccaactatag tttatattac atattttcaa 560

35 aaaccaataa aaattcctta tcttt 585

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<210> 30
 <211> 1100
 <212> DNA
 5 <213> Homo sapiens
 <220>
 <221> CDS
 <222> (57)...(1040)

10 <400> 30
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 Met
 1
 gcc gag ctc ccg ggg ccc ttt ctc tgc ggg gcc ctg cta ggc ttc ctg 107
 15 Ala Glu Leu Pro Gly Pro Phe Leu Cys Gly Ala Leu Leu Gly Phe Leu
 5 10 15
 tgc ctg agt ggg ctg gcc gtg gag gtg aag gta ccc aca gag ccg ctg 155
 Cys Leu Ser Gly Leu Ala Val Glu Val Lys Val Pro Thr Glu Pro Leu
 20 25 30
 20 agc acg ccc ctg ggg aag aca gcc gag ctg acc tgc acc tac agc acg 203
 Ser Thr Pro Leu Gly Lys Thr Ala Glu Leu Thr Cys Thr Tyr Ser Thr
 35 40 45
 tcg gtg gga gac agc ttc gcc ctg gag tgg agc ttt gtg cag cct ggg 251
 Ser Val Gly Asp Ser Phe Ala Leu Glu Trp Ser Phe Val Gln Pro Gly
 25 50 55 60 65
 aaa ccc atc tct gag tcc cat cca atc ctg tac ttc acc aat ggc cat 299
 Lys Pro Ile Ser Glu Ser His Pro Ile Leu Tyr Phe Thr Asn Gly His
 70 75 80
 ctg tat cca act ggt tct aag tca aag cgg gtc agc ctg ctt cag aac 347
 30 Leu Tyr Pro Thr Gly Ser Lys Ser Lys Arg Val Ser Leu Leu Gln Asn
 85 90 95
 ccc ccc aca gtg ggg gtg gcc aca ctg aaa ctg act gac gtc cac ccc 395
 Pro Pro Thr Val Gly Val Ala Thr Leu Lys Leu Thr Asp Val His Pro
 100 105 110
 35 tca gat act gga acc tac ctc tgc caa gtc aac aac cca cca gat ttc 443

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	Ser Asp Thr Gly Thr Tyr Leu Cys Gln Val Asn Asn Pro Pro Asp Phe	
	115 120 125	
	tac acc aat ggg ttg ggg cta atc aac ctt act gtg ctg gtt ccc ccc	491
	Tyr Thr Asn Gly Leu Gly Leu Ile Asn Leu Thr Val Leu Val Pro Pro	
5	130 135 140 145	
	agt aat ccc tta tgc agt cag agt gga caa acc tct gtg gga ggc tct	539
	Ser Asn Pro Leu Cys Ser Gln Ser Gly Gln Thr Ser Val Gly Gly Ser	
	150 155 160	
	act gca ctg aga tgc agc tct tcc gag ggg gct cct aag cca gtg tac	587
10	Thr Ala Leu Arg Cys Ser Ser Ser Glu Gly Ala Pro Lys Pro Val Tyr	
	165 170 175	
	aac tgg gtg cgt ctt gga act ttt cct aca cct tct cct ggc agc atg	635
	Asn Trp Val Arg Leu Gly Thr Phe Pro Thr Pro Ser Pro Gly Ser Met	
	180 185 190	
15	gtt caa gat gag gtg tct ggc cag ctc att ctc acc aac ctc tcc ctg	683
	Val Gln Asp Glu Val Ser Gly Gln Leu Ile Leu Thr Asn Leu Ser Leu	
	195 200 205	
	acc tcc tgc ggc acc tac cgc tgt gtg gcc acc aac cag atg ggc agt	731
	Thr Ser Ser Gly Thr Tyr Arg Cys Val Ala Thr Asn Gln Met Gly Ser	
20	210 215 220 225	
	gca tcc tgt gag ctg acc ctc tct gtg acc gaa ccc tcc caa ggc cga	779
	Ala Ser Cys Glu Leu Thr Leu Ser Val Thr Glu Pro Ser Gln Gly Arg	
	230 235 240	
	gtg gcc gga gct ctg att ggg gtg ctc ctg ggc gtg ctg ttg ctg tca	827
25	Val Ala Gly Ala Leu Ile Gly Val Leu Leu Gly Val Leu Leu Ser	
	245 250 255	
	gtt gct gcg ttc tgc ctg gtc agg ttc cag aaa gag agg ggg aag aag	875
	Val Ala Ala Phe Cys Leu Val Arg Phe Gln Lys Glu Arg Gly Lys Lys	
	260 265 270	
30	ccc aag gag aca tat ggg ggt agt gac ctt cgg gag gat gcc atc gct	923
	Pro Lys Glu Thr Tyr Gly Gly Ser Asp Leu Arg Glu Asp Ala Ile Ala	
	275 280 285	
	cct ggg atc tct gag cac act tgt atg agg gct gat tct agc aag ggg	971
	Pro Gly Ile Ser Glu His Thr Cys Met Arg Ala Asp Ser Ser Lys Gly	
35	290 295 300 305	

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ttc ctg gaa aga ccc tcg tct gcc agc acc gtg acg acc acc aag tcc 1019
 Phe Leu Glu Arg Pro Ser Ser Ala Ser Thr Val Thr Thr Thr Lys Ser
 310 315 320
 aag ctc cct atg gtc gtg tgactttctcc cgatccctga gggcgggtgag ggg 1070
 5 Lys Leu Pro Met Val Val
 325
 gaatatcaat aattaaagtc tgtgggtacc 1100

 <210> 31
 10 <211> 313
 <212> PRT
 <213> Homo sapiens

 <400> 31
 15 Met Asn Gln Leu Ser Phe Leu Leu Phe Leu Ile Ala Thr Thr Arg Gly
 1 5 10 15
 Trp Ser Thr Asp Glu Ala Asn Thr Tyr Phe Lys Glu Trp Thr Cys Ser
 20 25 30
 Ser Ser Pro Ser Leu Pro Arg Ser Cys Lys Glu Ile Lys Asp Glu Cys
 20 35 40 45
 Pro Ser Ala Phe Asp Gly Leu Tyr Phe Leu Arg Thr Glu Asn Gly Val
 50 55 60
 Ile Tyr Gln Thr Phe Cys Asp Met Thr Ser Gly Gly Gly Gly Trp Thr
 65 70 75 80
 25 Leu Val Ala Ser Val His Glu Asn Asp Met Arg Gly Lys Cys Thr Val
 85 90 95
 Gly Asp Arg Trp Ser Ser Gln Gln Gly Ser Lys Ala Asp Tyr Pro Glu
 100 105 110
 Gly Asp Gly Asn Trp Ala Asn Tyr Asn Thr Phe Gly Ser Ala Glu Ala
 115 120 125
 30 Ala Thr Ser Asp Asp Tyr Lys Asn Pro Gly Tyr Tyr Asp Ile Gln Ala
 130 135 140
 Lys Asp Leu Gly Ile Trp His Val Pro Asn Lys Ser Pro Met Gln His
 145 150 155 160
 35 Trp Arg Asn Ser Ser Leu Leu Arg Tyr Arg Thr Asp Thr Gly Phe Leu

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165 170 175
 Gln Thr Leu Gly His Asn Leu Phe Gly Ile Tyr Gln Lys Tyr Pro Val
 180 185 190
 Lys Tyr Gly Glu Gly Lys Cys Trp Thr Asp Asn Gly Pro Val Ile Pro
 5 195 200 205
 Val Val Tyr Asp Phe Gly Asp Ala Gln Lys Thr Ala Ser Tyr Tyr Ser
 210 215 220
 Pro Tyr Gly Gln Arg Glu Phe Thr Ala Gly Phe Val Gln Phe Arg Val
 225 230 235 240
 10 Phe Asn Asn Glu Arg Ala Ala Asn Ala Leu Cys Ala Gly Met Arg Val
 245 250 255
 Thr Gly Cys Asn Thr Glu His His Cys Ile Gly Gly Gly Tyr Phe
 260 265 270
 Pro Glu Ala Ser Pro Gln Gln Cys Gly Asp Phe Ser Gly Phe Asp Trp
 15 275 280 285
 Ser Gly Tyr Gly Thr His Val Gly Tyr Ser Ser Ser Arg Glu Ile Thr
 290 295 300
 Glu Ala Ala Val Leu Leu Phe Tyr Arg
 305 310
 20
 <210> 32
 <211> 229
 <212> PRT
 <213> Homo sapiens
 25
 <400> 32
 Met Gly Asp Lys Ile Trp Leu Pro Phe Pro Val Leu Leu Leu Ala Ala
 1 5 10 15
 Leu Pro Pro Val Leu Leu Pro Gly Ala Ala Gly Phe Thr Pro Ser Leu
 30 20 25 30
 Asp Ser Asp Phe Thr Phe Thr Leu Pro Ala Gly Gln Lys Glu Cys Phe
 35 40 45
 Tyr Gln Pro Met Pro Leu Lys Ala Ser Leu Glu Ile Glu Tyr Gln Val
 50 55 60
 35 Leu Asp Gly Ala Gly Leu Asp Ile Asp Phe His Leu Ala Ser Pro Glu

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65 70 75 80
 Gly Lys Thr Leu Val Phe Glu Gln Arg Lys Ser Asp Gly Val His Thr
 85 90 95
 Val Glu Thr Glu Val Gly Asp Tyr Met Phe Cys Phe Asp Asn Thr Phe
 5 100 105 110
 Ser Thr Ile Ser Glu Lys Val Ile Phe Phe Glu Leu Ile Leu Asp Asn
 115 120 125
 Met Gly Glu Gln Ala Gln Glu Gln Glu Asp Trp Lys Lys Tyr Ile Thr
 130 135 140
 10 Gly Thr Asp Ile Leu Asp Met Lys Leu Glu Asp Ile Leu Glu Ser Ile
 145 150 155 160
 Asn Ser Ile Lys Ser Arg Leu Ser Lys Ser Gly His Ile Gln Ile Leu
 165 170 175
 Leu Arg Ala Phe Glu Ala Arg Asp Arg Asn Ile Gln Glu Ser Asn Phe
 15 180 185 190
 Asp Arg Val Asn Phe Trp Ser Met Val Asn Leu Val Val Met Val Val
 195 200 205
 Val Ser Ala Ile Gln Val Tyr Met Leu Lys Ser Leu Phe Glu Asp Lys
 210 215 220
 20 Arg Lys Ser Arg Thr
 225

 <210> 33
 <211> 467
 25 <212> PRT
 <213> Homo sapiens

 <400> 33
 Met Arg Pro Gln Glu Leu Pro Arg Leu Ala Phe Pro Leu Leu Leu Leu
 30 1 5 10 15
 Leu Leu Leu Leu Leu Pro Pro Pro Pro Cys Pro Ala His Ser Ala Thr
 20 25 30
 Arg Phe Asp Pro Thr Trp Glu Ser Leu Asp Ala Arg Gln Leu Pro Ala
 35 40 45
 35 Trp Phe Asp Gln Ala Lys Phe Gly Ile Phe Ile His Trp Gly Val Phe

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	50		55		60
	Ser Val Pro Ser Phe Gly Ser Glu Trp Phe Trp Trp Tyr Trp Gln Lys				
	65		70		75 80
5	Glu Lys Ile Pro Lys Tyr Val Glu Phe Met Lys Asp Asn Tyr Pro Pro				
		85		90	95
	Ser Phe Lys Tyr Glu Asp Phe Gly Pro Leu Phe Thr Ala Lys Phe Phe				
		100		105	110
	Asn Ala Asn Gln Trp Ala Asp Ile Phe Gln Ala Ser Gly Ala Lys Tyr				
		115		120	125
10	Ile Val Leu Thr Ser Lys His His Glu Gly Phe Thr Leu Trp Gly Ser				
		130		135	140
	Glu Tyr Ser Trp Asn Trp Asn Ala Ile Asp Glu Gly Pro Lys Arg Asp				
		145		150	155 160
	Ile Val Lys Glu Leu Glu Val Ala Ile Arg Asn Arg Thr Asp Leu Arg				
15		165		170	175
	Phe Gly Leu Tyr Tyr Ser Leu Phe Glu Trp Phe His Pro Leu Phe Leu				
		180		185	190
	Glu Asp Glu Ser Ser Ser Phe His Lys Arg Gln Phe Pro Val Ser Lys				
		195		200	205
20	Thr Leu Pro Glu Leu Tyr Glu Leu Val Asn Asn Tyr Gln Pro Glu Val				
		210		215	220
	Leu Trp Ser Asp Gly Asp Gly Gly Ala Pro Asp Gln Tyr Trp Asn Ser				
		225		230	235 240
	Thr Gly Phe Leu Ala Trp Leu Tyr Asn Glu Ser Pro Val Arg Gly Thr				
25		245		250	255
	Val Val Thr Asn Asp Arg Trp Gly Ala Gly Ser Ile Cys Lys His Gly				
		260		265	270
	Gly Phe Tyr Thr Cys Ser Asp Arg Tyr Asn Pro Gly His Leu Leu Pro				
		275		280	285
30	His Lys Trp Glu Asn Cys Met Thr Ile Asp Lys Leu Ser Trp Gly Tyr				
		290		295	300
	Arg Arg Glu Ala Gly Ile Ser Asp Tyr Leu Thr Ile Glu Glu Leu Val				
		305		310	315 320
	Lys Gln Leu Val Glu Thr Val Ser Cys Gly Gly Asn Leu Leu Met Asn				
35		325		330	335

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Ile Gly Pro Thr Leu Asp Gly Thr Ile Ser Val Val Phe Glu Glu Arg
 340 345 350
 Leu Arg Gln Met Gly Ser Trp Leu Lys Val Asn Gly Glu Ala Ile Tyr
 355 360 365
 5 Glu Thr His Thr Trp Arg Ser Gln Asn Asp Thr Val Thr Pro Asp Val
 370 375 380
 Trp Tyr Thr Ser Lys Pro Lys Glu Lys Leu Val Tyr Ala Ile Phe Leu
 385 390 395 400
 Lys Trp Pro Thr Ser Gly Gln Leu Phe Leu Gly His Pro Lys Ala Ile
 10 405 410 415
 Leu Gly Ala Thr Glu Val Lys Leu Leu Gly His Gly Gln Pro Leu Asn
 420 425 430
 Trp Ile Ser Leu Glu Gln Asn Gly Ile Met Val Glu Leu Pro Gln Leu
 435 440 445
 15 Thr Ile His Gln Met Pro Cys Lys Trp Gly Trp Ala Leu Ala Leu Thr
 450 455 460
 Asn Val Ile
 465

 20 <210> 34
 <211> 99
 <212> PRT
 <213> Homo sapiens

 25 <400> 34
 Met Asp Asn Val Gln Pro Lys Ile Lys His Arg Pro Phe Cys Phe Ser
 1 5 10 15
 Val Lys Gly His Val Lys Met Leu Arg Leu Asp Ile Ile Asn Ser Leu
 20 25 30
 30 Val Thr Thr Val Phe Met Leu Ile Val Ser Val Leu Ala Leu Ile Pro
 35 40 45
 Glu Thr Thr Thr Leu Thr Val Gly Gly Gly Val Phe Ala Leu Val Thr
 50 55 60
 Ala Val Cys Cys Leu Ala Asp Gly Ala Leu Ile Tyr Arg Lys Leu Leu
 35 65 70 75 80

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Phe Asn Pro Ser Gly Pro Tyr Gln Gln Lys Pro Val His Glu Lys Lys
 85 90 95

Glu Val Leu

5 <210> 35

<211> 189

<212> PRT

<213> Homo sapiens

10 <400> 35

Met Glu Glu Gly Gly Asn Leu Gly Gly Leu Ile Lys Met Val His Leu
 1 5 10 15

Leu Val Leu Ser Gly Ala Trp Gly Met Gln Met Trp Val Thr Phe Val
 20 25 30

15 Ser Gly Phe Leu Leu Phe Arg Ser Leu Pro Arg His Thr Phe Gly Leu
 35 40 45

Val Gln Ser Lys Leu Phe Pro Phe Tyr Phe His Ile Ser Met Gly Cys
 50 55 60

20 Ala Phe Ile Asn Leu Cys Ile Leu Ala Ser Gln His Ala Trp Ala Gln
 65 70 75 80

Leu Thr Phe Trp Glu Ala Ser Gln Leu Tyr Leu Leu Phe Leu Ser Leu
 85 90 95

Thr Leu Ala Thr Val Asn Ala Arg Trp Leu Glu Pro Arg Thr Thr Ala
 100 105 110

25 Ala Met Trp Ala Leu Gln Thr Val Glu Lys Glu Arg Gly Leu Gly Gly
 115 120 125

Glu Val Pro Gly Ser His Gln Gly Pro Asp Pro Tyr Arg Gln Leu Arg
 130 135 140

30 Glu Lys Asp Pro Lys Tyr Ser Ala Leu Arg Gln Asn Phe Phe Arg Tyr
 145 150 155 160

His Gly Leu Ser Ser Leu Cys Asn Leu Gly Cys Val Leu Ser Asn Gly
 165 170 175

Leu Cys Leu Ala Gly Leu Ala Leu Glu Ile Arg Ser Leu
 180 185

35

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<210> 36

<211> 363

<212> PRT

<213> Homo sapiens

5

<400> 36

Met Val Asp Ser Leu Leu Ala Val Thr Leu Ala Gly Asn Leu Gly Leu
 1 5 10 15
 Thr Phe Leu Arg Gly Ser Gln Thr Gln Ser His Pro Asp Leu Gly Thr
 10 20 25 30
 Glu Gly Cys Trp Asp Gln Leu Ser Ala Pro Arg Thr Phe Thr Leu Leu
 35 40 45
 Asp Pro Lys Ala Ser Leu Leu Thr Lys Ala Phe Leu Asn Gly Ala Leu
 50 55 60
 15 Asp Gly Val Ile Leu Gly Asp Tyr Leu Ser Arg Thr Pro Glu Pro Arg
 65 70 75 80
 Pro Ser Leu Ser His Leu Leu Ser Gln Tyr Tyr Gly Ala Gly Val Ala
 85 90 95
 Arg Asp Pro Gly Phe Arg Ser Asn Phe Arg Arg Gln Asn Gly Ala Ala
 100 105 110
 20 Leu Thr Ser Ala Ser Ile Leu Ala Gln Gln Val Trp Gly Thr Leu Val
 115 120 125
 Leu Leu Gln Arg Leu Glu Pro Val His Leu Gln Leu Gln Cys Met Ser
 130 135 140
 25 Gln Glu Gln Leu Ala Gln Val Ala Ala Asn Ala Thr Lys Glu Phe Thr
 145 150 155 160
 Glu Ala Phe Leu Gly Cys Pro Ala Ile His Pro Arg Cys Arg Trp Gly
 165 170 175
 Ala Ala Pro Tyr Arg Gly Arg Pro Lys Leu Leu Gln Leu Pro Leu Gly
 180 185 190
 30 Phe Leu Tyr Val His His Thr Tyr Val Pro Ala Pro Pro Cys Thr Asp
 195 200 205
 Phe Thr Arg Cys Ala Ala Asn Met Arg Ser Met Gln Arg Tyr His Gln
 210 215 220
 35 Asp Thr Gln Gly Trp Gly Asp Ile Gly Tyr Ser Phe Val Val Gly Ser

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225 230 235 240
 Asp Gly Tyr Val Tyr Glu Gly Arg Gly Trp His Trp Val Gly Ala His
 245 250 255
 Thr Leu Gly His Asn Ser Arg Gly Phe Gly Val Ala Ile Val Gly Asn
 5 260 265 270
 Tyr Thr Ala Ala Leu Pro Thr Glu Ala Ala Leu Arg Thr Val Arg Asp
 275 280 285
 Thr Leu Pro Ser Cys Ala Val Arg Ala Gly Leu Leu Arg Pro Asp Tyr
 290 295 300
 10 Ala Leu Leu Gly His Arg Gln Leu Val Arg Thr Asp Cys Pro Gly Asp
 305 310 315 320
 Ala Leu Phe Asp Leu Leu Arg Thr Trp Pro His Phe Thr Ala Thr Val
 325 330 335
 Lys Pro Arg Pro Ala Arg Ser Val Ser Lys Arg Ser Arg Arg Glu Pro
 15 340 345 350
 Pro Pro Arg Thr Leu Pro Ala Thr Asp Leu Gln
 355 360

 <210> 37
 20 <211> 249
 <212> PRT
 <213> Homo sapiens

 <400> 37
 25 Met Gly Gly Pro Arg Gly Ala Gly Trp Val Ala Ala Gly Leu Leu Leu
 1 5 10 15
 Gly Ala Gly Ala Cys Tyr Cys Ile Tyr Arg Leu Thr Arg Gly Arg Arg
 20 25 30
 Arg Gly Asp Arg Glu Leu Gly Ile Arg Ser Ser Lys Ser Ala Glu Asp
 30 35 40 45
 Leu Thr Asp Gly Ser Tyr Asp Asp Val Leu Asn Ala Glu Gln Leu Gln
 50 55 60
 Lys Leu Leu Tyr Leu Leu Glu Ser Thr Glu Asp Pro Val Ile Ile Glu
 65 70 75 80
 35 Arg Ala Leu Ile Thr Leu Gly Asn Asn Ala Ala Phe Ser Val Asn Gln

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	85	90	95
	Ala Ile Ile Arg Glu Leu Gly Gly Ile Pro Ile Val Ala Asn Lys Ile		
	100	105	110
	Asn His Ser Asn Gln Ser Ile Lys Glu Lys Ala Leu Asn Ala Leu Asn		
5	115	120	125
	Asn Leu Ser Val Asn Val Glu Asn Gln Ile Lys Ile Lys Val Gln Val		
	130	135	140
	Leu Lys Leu Leu Leu Asn Leu Ser Glu Asn Pro Ala Met Thr Glu Gly		
	145	150	155
10	Leu Leu Arg Ala Gln Val Asp Ser Ser Phe Leu Ser Leu Tyr Asp Ser		
	165	170	175
	His Val Ala Lys Glu Ile Leu Leu Arg Val Leu Thr Leu Phe Gln Asn		
	180	185	190
	Ile Lys Asn Cys Leu Lys Ile Glu Gly His Leu Ala Val Gln Pro Thr		
15	195	200	205
	Phe Thr Glu Gly Ser Leu Phe Phe Leu Leu His Gly Glu Glu Cys Ala		
	210	215	220
	Gln Lys Ile Arg Ala Leu Val Asp His His Asp Ala Glu Val Lys Glu		
	225	230	235
20	Lys Val Val Thr Ile Ile Pro Lys Ile		
	245		
	<210> 38		
	<211> 98		
25	<212> PRT		
	<213> Homo sapiens		
	<400> 38		
	Met Ala Ser Leu Leu Cys Cys Gly Pro Lys Leu Ala Ala Cys Gly Ile		
30	1	5	10
	Val Leu Ser Ala Trp Gly Val Ile Met Leu Ile Met Leu Gly Ile Phe		
	20	25	30
	Phe Asn Val His Ser Ala Val Leu Ile Glu Asp Val Pro Phe Thr Glu		
	35	40	45
35	Lys Asp Phe Glu Asn Gly Pro Gln Asn Ile Tyr Asn Leu Tyr Glu Gln		

```

      50              55              60
Val Ser Tyr Asn Cys Phe Ile Ala Ala Gly Leu Tyr Leu Leu Leu Gly
      65              70              75              80
Gly Phe Ser Phe Cys Gln Val Arg Leu Asn Lys Arg Lys Glu Tyr Met
5              85              90              95
Val Arg

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<210> 39
<211> 172
<212> PRT
<213> Homo sapiens
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	Met	Val	Gly	Pro	Ala	Pro	Arg	Arg	Arg	Leu	Arg	Pro	Leu	Ala	Ala	Leu
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	Ala	Leu	Val	Leu	Ala	Leu	Ala	Pro	Gly	Leu	Pro	Thr	Ala	Arg	Ala	Gly
				20					25					30		
	Gln	Thr	Pro	Arg	Pro	Ala	Glu	Arg	Gly	Pro	Pro	Val	Arg	Leu	Phe	Thr
			35					40					45			
20	Glu	Glu	Glu	Leu	Ala	Arg	Tyr	Gly	Gly	Glu	Glu	Glu	Asp	Gln	Pro	Ile
		50					55					60				
	Tyr	Leu	Ala	Val	Lys	Gly	Val	Val	Phe	Asp	Val	Thr	Ser	Gly	Lys	Glu
	65					70					75				80	
	Phe	Tyr	Gly	Arg	Gly	Ala	Pro	Tyr	Asn	Ala	Leu	Thr	Gly	Lys	Asp	Ser
25					85					90					95	
	Thr	Arg	Gly	Val	Ala	Lys	Met	Ser	Leu	Asp	Pro	Ala	Asp	Leu	Thr	His
				100					105					110		
	Asp	Thr	Thr	Gly	Leu	Thr	Ala	Lys	Glu	Leu	Glu	Ala	Leu	Asp	Glu	Val
			115					120					125			
30	Phe	Thr	Lys	Val	Tyr	Lys	Ala	Lys	Tyr	Pro	Ile	Val	Gly	Tyr	Thr	Ala
		130					135					140				
	Arg	Arg	Ile	Leu	Asn	Glu	Asp	Gly	Ser	Pro	Asn	Leu	Asp	Phe	Lys	Pro
	145					150					155				160	
	Glu	Asp	Gln	Pro	His	Phe	Asp	Ile	Lys	Asp	Glu	Phe				
35					165					170						

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<210> 40
 <211> 120
 <212> PRT
 5 <213> Homo sapiens

<400> 40
 Met Met Pro Ser Arg Thr Asn Leu Ala Thr Gly Ile Pro Ser Ser Lys
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 10 Val Lys Tyr Ser Arg Leu Ser Ser Thr Asp Asp Gly Tyr Ile Asp Leu
 20 25 30
 Gln Phe Lys Lys Thr Pro Pro Lys Ile Pro Tyr Lys Ala Ile Ala Leu
 35 40 45
 Ala Thr Val Leu Phe Leu Ile Gly Ala Phe Leu Ile Ile Ile Gly Ser
 15 50 55 60
 Leu Leu Leu Ser Gly Tyr Ile Ser Lys Gly Gly Ala Asp Arg Ala Val
 65 70 75 80
 Pro Val Leu Ile Ile Gly Ile Leu Val Phe Leu Pro Gly Phe Tyr His
 85 90 95
 20 Leu Arg Ile Ala Tyr Tyr Ala Ser Lys Gly Tyr Arg Gly Tyr Ser Tyr
 100 105 110
 Asp Asp Ile Pro Asp Phe Asp Asp
 115 120

25 <210> 41
 <211> 939
 <212> DNA
 <213> Homo sapiens

30 <400> 41
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 gaggetaata cttacttcaa ggaatggacc tgttcttcgt ctccatctct gccagaagc 120
 tgcaaggaaa tcaaagacga atgtcctagt gcatttgatg gcctgtattt tctccgcact 180
 gagaatggtg ttatctacca gaccttctgt gacatgacct ctgggggtgg cggtcgacc 240
 35 ctggtggcca gcgtgcatga gaatgacatg cgtgggaagt gcacgggtgg cgatcgctgg 300

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	tccagtcagc agggcagcaa agcagactac ccagaggggg acggcaactg ggccaactac	360
	aacacctttg gatctgcaga ggcggccacg agcgatgact acaagaaccc tggctactac	420
	gacatccagg ccaaggacct gggcatctgg cacgtgceca ataagtcctc catgcagcac	480
	tggagaaaca gctccctgct gaggtaccgc acggacactg gcttcctcca gacactggga	540
5	cataatctgt ttggcatcta ccagaaatat ccagtgaat atggagaagg aaagtgttgg	600
	actgacaacg gcccggtgat ccctgtggtc tatgattttg gcgacgceca gaaaacagca	660
	tottattact caccctatgg ccagcgggaa ttcactgcgg gatttgttca gttcagggta	720
	tttaataacg agagagcagc caacgccttg tgtgctggaa tgagggtcac cggatgtaac	780
	actgagcacc actgcattgg tggaggagga tactttccag aggccagtcc ccagcagtgt	840
10	ggagatTTTT ctggttttga ttggagtgga tatggaactc atgttggtta cagcagcagc	900
	cgtgagataa ctgaggcagc tgtgcttcta ttctatcgt	939
	<210> 42	
	<211> 687	
15	<212> DNA	
	<213> Homo sapiens	
	<400> 42	
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20	ctgtgcctg gggcggccgg cttcacacct tccctcgata gcgacttcac ctttaccctt	120
	cccgcgggcc agaaggagt cttctaccag cccatgcccc tgaaggcctc gctggagatc	180
	gagtaccaag ttttagatgg agcaggatta gatattgatt tccatcttgc ctctccagaa	240
	ggcaaacct tagtTTTTga acaagaaaa tcagatggag ttcacactgt agagactgaa	300
	gttggtgatt acatgttctg ctttgacaat acattcagca ccatttctga gaagggtgatt	360
25	ttctttgaat taatcctgga taatatggga gaacaggcac aagaacaaga agattggaag	420
	aaatatatta ctggcacaga tatattggat atgaaactgg aagacatcct ggaatccatc	480
	aacagcatca agtccagact aagcaaaagt gggcacatac aaattctgct tagagcattt	540
	gaagctcgtg atcgaaacat acaagaaagc aactttgata gagtcaattt ctggtctatg	600
	gttaatttag tggatcatggt ggtggtgtca gccattcaag tttatatgct gaagagtctg	660
30	tttgaagata agaggaaaag tagaact	687
	<210> 43	
	<211> 1401	
	<212> DNA	
35	<213> Homo sapiens	

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<400> 43

	atgcggcccc	aggagctccc	caggctcgcg	ttcccggtgc	tgtgtgtgct	gttgtgtgctg	60
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5	ctggacgccc	gccagctgcc	cgcgtggtt	gaccaggcca	agttcggcat	cttcatccac	180
	tggggagtg	ttccggtgcc	cagcttcggt	agcgagtgg	tctggtggt	ttggcaaaag	240
	gaaaagatac	cgaagtatgt	ggaatttatg	aaagataatt	accctcctag	tttcaaatat	300
	gaagattttg	gaccactatt	tacagcaaaa	ttttttaatg	ccaaccagt	ggcagatatt	360
	tttcaggcct	ctggtgccaa	atacattgtc	ttaacttcca	aacatcatga	aggctttacc	420
10	ttgtgggggt	cagaatatcc	gtggaactgg	aatgccatag	atgaggggccc	caagagggac	480
	attgtcaagg	aacttgaggt	agccattagg	aacagaactg	acctgcgttt	tggactgtac	540
	tattcccttt	ttgaatgggt	tcacccgctc	ttccttgagg	atgaatccag	ttcattccat	600
	aagcggcaat	ttccagtttc	taagacattg	ccagagctct	atgagttagt	gaacaactat	660
	cagcctgagg	ttctgtggtc	ggatggtgac	ggaggagcac	cggatcaata	ctggaacagc	720
15	acaggcttct	tggcctgggt	atataatgaa	agcccagttc	ggggcacagt	agtcaccaat	780
	gatcggtggg	gagctggtag	catctgtaag	catggtggct	tctataacctg	cagtgatcgt	840
	tataaccacg	gacatctttt	gccacataaa	tgggaaaact	gcatgacaat	agacaaaactg	900
	tcctggggct	ataggaggga	agctggaatc	tctgactatc	ttacaattga	agaattgggtg	960
	aagcaacttg	tagagacagt	ttcatgtgga	ggaaatcttt	tgatgaatat	tgggcccaca	1020
20	ctagatggca	ccattttctgt	agtttttgag	gagcgactga	ggcaaatggg	gtcctggcta	1080
	aaagtcaatg	gagaagctat	ttatgaaacc	catacctggc	gatcccagaa	tgacactgtc	1140
	accccagatg	tgtggtacac	atccaagcct	aaagaaaaat	tagtctatgc	catttttctt	1200
	aatggccca	catcaggaca	gctgttcctt	ggccatccca	aagctattct	gggggcaaca	1260
	gaggtgaaac	tactgggcca	tggacagcca	cttaactgga	tttctttgga	gcaaaatggc	1320
25	attatggtag	aactgccaca	gctaaccatt	catcagatgc	cgtgtaaag	gggctgggct	1380
	ctagccctga	ctaattgtgat	c				1401

<210> 44

<211> 297

30 <212> DNA

<213> Homo sapiens

<400> 44

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35	gtgaagatgc	tgcggctgga	tattatcaac	tcactggtaa	caacagtatt	catgctcatc	120

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gtatctgtgt tggcactgat accagaaacc acaacattga cagttggtgg aggggtgttt 180
gcacttgatg cagcagtatg ctgtcttgcc gacggggccc ttatttaccg gaagcttctg 240
ttcaatccca gcggtcetta ccagcaaaag cctgtgcatg aaaaaaaga agttttg 297

5 <210> 45
<211> 567
<212> DNA
<213> Homo sapiens

10 <400> 45
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ggtgcctggg gcatgcaaatt gtgggtgacc ttcgtctcag gcttctctgt ttcccgaaagc 120
cttccccgac ataccttcgg actagtgcag agcaaactct tccccctcta cttccacatc 180
tccatgggct gtgccttcat caacctctgc atcttggett cacagcatgc ttgggctcag 240
.15 ctcacattct gggaggccag ccagctttac ctgctgttcc tgagccttac gctggccact 300
gtcaacgccc gctggctgga accccgcacc acagctgcca tgtgggccct gcaaaccgtg 360
gagaaggagc gaggcctggg tggggaggta ccaggcagcc accagggtcc cgatccctac 420
cgccagctgc gagagaagga ccccaagtac agtgcctctc gccagaattt cttccgctac 480
catgggctgt cctctctttg caatctgggc tgcgtcctga gcaatgggct ctgtctcgtc 540
20 ggccttgccc tggaaataag gagectc 567

<210> 46
<211> 1089
<212> DNA

25 <213> Homo sapiens

<400> 46
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ggttcccaga cccagagcca tccagacctg ggaactgagg gctgctggga ccagctctct 120
30 gcccctcgga cttttacgtt tttggacccc aaggcatctc tgtaaccaa ggccttctc 180
aatggcgccc tggatggggt catccttgga gactacctga gccggactcc tgagccccgg 240
ccatccctca gccacttgct gagccagtac tatggggctg ggggtggccag agaccaggg 300
ttccgcagca acttccgacg gcagaacggg gctgctctga cttcagcctc catcctggcc 360
cagcaggtgt ggggaaccct tgccttctta cagaggtgg agccagtaca cctccagctt 420
35 cagtgcata gccaagaaca gctggcccag gtggctgcca atgctaccaa ggaattcact 480

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	gaggccttcc tgggatgccc ggccatccac ccccgctgcc gctggggagc ggcgccttat	540
	cggggcgccc cgaagctgct gcagctgccg ctgggattct tgtacgtgca tcacacctac	600
	gtgcctgcac caccctgcac ggacttcacg cgctgcgcag ccaacatgcg ctccatgcag	660
	cgtaccacc aggacacgca aggctgggga gacatcggt acagtttcgt ggtgggctcg	720
5	gacggctacg tgtacgaggg acgcggctgg cactgggtgg gcgcccacac gctcggccac	780
	aactcccggg gcttcggcgt ggccatagtg ggcaactaca ccgcggcgct gccaccgcag	840
	gccgctctgc gcacgggtgc cgacacgctc ccgagttgtg cgggtgcgcgc cggcctcctg	900
	cggccagact acgcgctgct gggccaccgc cagctgggtgc gcaccgactg ccccggcgac	960
	gcgctcttcg acctgctgcg cacctggccg cacttcaccg cgactgttaa gccaaacct	1020
10	gccaggagtg tctctaagag atccaggagg gagccacccc caaggaccct gccagccaca	1080
	gacctccaa	1089
	<210> 47	
	<211> 747	
15	<212> DNA	
	<213> Homo sapiens	
	<400> 47	
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20	tgetactgca ttacaggct gacccggggt cggcggcggg gcgaccgca gctcgggata	120
	cgtcttcga agtcgcaga agacttaact gatggttcat atgatgatgt tctaaatget	180
	gaacaacttc agaaactcct ttacctgctg gagtcaacgg aggatcctgt aattattgaa	240
	agagctttga ttactttggg taacaatgca gccttttcag ttaaccaagc tattattcgt	300
	gaattgggtg gtattccaat tgttgcaaac aaaatcaacc attccaacca gagtattaaa	360
25	gagaaagctt taaatgcact aaataacctg agtgtgaatg ttgaaaatca aatcaagata	420
	aagggtgcaag ttttgaaact gcttttgaat ttgtctgaaa atccagccat gacagaagga	480
	cttctccgtg cccaagtgga ttcattcatt ctttcccttt atgacagcca cgtagcaaag	540
	gagattcttc ttcgagtact tacgctatct cagaatataa agaactgcct caaaatagaa	600
	ggccatttag ctgtgcagcc tactttcact gaaggttcat tgtttttcct gttacatgga	660
30	gaagaatgtg ccagaaaaat aagagcttta gttgatcacc atgatgcaga ggtgaaggaa	720
	aaggttgtaa caataatacc caaaatc	747
	<210> 48	
	<211> 294	
35	<212> DNA	

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<213> Homo sapiens

<400> 48

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 tggggagtga tcatgttgat aatgctcgga atatttttca atgtccattc cgctgtgttg 120
 attgaggacg ttcccttcac ggagaaagat tttgagaatg gccccagaa catatacaac 180
 ctttacgagc aagtcageta caactgtttc atcgctgcag gcctttacct cctcctcgga 240
 ggcttctctt tctgccaagt tcggctcaat aagcgcaagg aatacatggt gcgc 294

10 <210> 49

<211> 516

<212> DNA

<213> Homo sapiens

15 <400> 49

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 gcgtggccc cggggctgcc cacagcccgg gccgggcaga caccgcgcc tgcgagcgg 120
 gggccccag tgcggctttt caccgaggag gagctggccc gctatggcgg ggaggaggaa 180
 gatcagccca tctacttgge agtgaagggg gtggtgtttg atgtcacctc cggaaaggag 240
 20 ttttatggac gaggagcccc ctacaatgcc ttgacgggga aggactccac tagaggggta 300
 gccaatgt ccttggatec tgcagacctc acctatgaca ctacgggtct caccggccaag 360
 gaactggagg ccttgatga ggtcttcacc aaagtgtaca aagccaaata cccatcgctc 420
 ggctacactg cccggagaat tctcaatgag gatggcagcc ctaacctgga cttcaagcct 480
 gaagaccagc cccattttga catcaaggat gaggttc 516

25

<210> 50

<211> 360

<212> DNA

<213> Homo sapiens

30

<400> 50

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 aggetctcca gcacagacga tggctacatt gaccttcagt ttaagaaaac ccctcctaag 120
 atcccttata aggccatcgc acttgccact gtgctgtttt tgattggcgc ctttctcatt 180
 35 attataggct ccctcctget gtcaggctac atcagcaaag ggggggcaga ccgggcegtt 240

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ccagtgc tga tcat tggcat tctggtgttc ctacccggat tttaccacct gcgcatoget 300
tactatgcat ccaaaggcta ccgtgggttac tctatgatg acattccaga ctttgatgac 360

<210> 51

5 <211> 1065

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

10 <222> (2)...(943)

<400> 51

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Met Asn Gln Leu Ser Phe Leu Leu Phe Leu Ile Ala Thr Thr Arg Gly
15 1 5 10 15
tgg agt aca gat gag gct aat act tac ttc aag gaa tgg acc tgt tct 97
Trp Ser Thr Asp Glu Ala Asn Thr Tyr Phe Lys Glu Trp Thr Cys Ser
20 20 25 30
tcg tct cca tct ctg ccc aga agc tgc aag gaa atc aaa gac gaa tgt 145
Ser Ser Pro Ser Leu Pro Arg Ser Cys Lys Glu Ile Lys Asp Glu Cys
35 40 45
cct agt gca ttt gat ggc ctg tat ttt ctc cgc act gag aat ggt gtt 193
Pro Ser Ala Phe Asp Gly Leu Tyr Phe Leu Arg Thr Glu Asn Gly Val
50 55 60
25 atc tac cag acc ttc tgt gac atg acc tct ggg ggt ggc ggc tgg acc 241
Ile Tyr Gln Thr Phe Cys Asp Met Thr Ser Gly Gly Gly Gly Trp Thr
65 70 75 80
ctg gtg gcc agc gtg cat gag aat gac atg cgt ggg aag tgc acg gtg 289
Leu Val Ala Ser Val His Glu Asn Asp Met Arg Gly Lys Cys Thr Val
30 85 90 95
ggc gat cgc tgg tcc agt cag cag ggc agc aaa gca gac tac cca gag 337
Gly Asp Arg Trp Ser Ser Gln Gln Gly Ser Lys Ala Asp Tyr Pro Glu
100 105 110
ggg gac ggc aac tgg gcc aac tac aac acc ttt gga tct gca gag gcg 385
35 Gly Asp Gly Asn Trp Ala Asn Tyr Asn Thr Phe Gly Ser Ala Glu Ala

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	115	120	125	
	gcc acg agc gat gac tac aag aac cct ggc tac tac gac atc cag gcc			433
	Ala Thr Ser Asp Asp Tyr Lys Asn Pro Gly Tyr Tyr Asp Ile Gln Ala			
	130	135	140	
5	aag gac ctg ggc atc tgg cac gtg ccc aat aag tcc ccc atg cag cac			481
	Lys Asp Leu Gly Ile Trp His Val Pro Asn Lys Ser Pro Met Gln His			
	145	150	155	160
	tgg aga aac agc tcc ctg ctg agg tac cgc acg gac act ggc ttc ctc			529
	Trp Arg Asn Ser Ser Leu Leu Arg Tyr Arg Thr Asp Thr Gly Phe Leu			
10	165	170	175	
	cag aca ctg gga cat aat ctg ttt ggc atc tac cag aaa tat cca gtg			577
	Gln Thr Leu Gly His Asn Leu Phe Gly Ile Tyr Gln Lys Tyr Pro Val			
	180	185	190	
	aaa tat gga gaa gga aag tgt tgg act gac aac ggc ccg gtg atc cct			625
15	Lys Tyr Gly Glu Gly Lys Cys Trp Thr Asp Asn Gly Pro Val Ile Pro			
	195	200	205	
	gtg gtc tat gat ttt ggc gac gcc cag aaa aca gca tct tat tac tca			673
	Val Val Tyr Asp Phe Gly Asp Ala Gln Lys Thr Ala Ser Tyr Tyr Ser			
	210	215	220	
20	ccc tat ggc cag cgg gaa ttc act gcg gga ttt gtt cag ttc agg gta			721
	Pro Tyr Gly Gln Arg Glu Phe Thr Ala Gly Phe Val Gln Phe Arg Val			
	225	230	235	240
	ttt aat aac gag aga gca gcc aac gcc ttg tgt gct gga atg agg gtc			769
	Phe Asn Asn Glu Arg Ala Ala Asn Ala Leu Cys Ala Gly Met Arg Val			
25	245	250	255	
	acc gga tgt aac act gag cac cac tgc att ggt gga gga gga tac ttt			817
	Thr Gly Cys Asn Thr Glu His His Cys Ile Gly Gly Gly Gly Tyr Phe			
	260	265	270	
	cca gag gcc agt ccc cag cag tgt gga gat ttt tct ggt ttt gat tgg			865
30	Pro Glu Ala Ser Pro Gln Gln Cys Gly Asp Phe Ser Gly Phe Asp Trp			
	275	280	285	
	agt gga tat gga act cat gtt ggt tac agc agc agc cgt gag ata act			913
	Ser Gly Tyr Gly Thr His Val Gly Tyr Ser Ser Ser Arg Glu Ile Thr			
	290	295	300	
35	gag gca gct gtg ctt cta ttc tat cgt tgagagtttt gtgggagggga			960

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Glu Ala Ala Val Leu Leu Phe Tyr Arg
 305 310
 acccagacct ctctcccaa ccatgagatc ccaaggatgg agaacaactt acccagtagc 1020
 tagaatgtta atggcagaag agaaaacaat aaatcatatt gactc 1065

5
 <210> 52
 <211> 937
 <212> DNA
 <213> Homo sapiens

10
 <220>
 <221> CDS
 <222> (177)...(866)

<400> 52

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 ggagcggaga caacagtacc tgacgcctct ttcagcccg gacgcgccca gcaggg 176
 atg ggc gac aag atc tgg ctg ccc ttc ccc gtg ctc ctt ctg gcc get 224
 Met Gly Asp Lys Ile Trp Leu Pro Phe Pro Val Leu Leu Leu Ala Ala

20
 1 5 10 15
 ctg cct ccg gtg ctg ctg cct ggg gcg gcc ggc ttc aca cct tcc ctc 272
 Leu Pro Pro Val Leu Leu Pro Gly Ala Ala Gly Phe Thr Pro Ser Leu
 20 25 30
 gat agc gac ttc acc ttt acc ctt ccc gcc ggc cag aag gag tgc ttc 320
 25
 Asp Ser Asp Phe Thr Phe Thr Leu Pro Ala Gly Gln Lys Glu Cys Phe
 35 40 45
 tac cag ccc atg ccc ctg aag gcc tcg ctg gag atc gag tac caa gtt 368
 Tyr Gln Pro Met Pro Leu Lys Ala Ser Leu Glu Ile Glu Tyr Gln Val
 50 55 60

30
 tta gat gga gca gga tta gat att gat ttc cat ctt gcc tct cca gaa 416
 Leu Asp Gly Ala Gly Leu Asp Ile Asp Phe His Leu Ala Ser Pro Glu
 65 70 75 80
 ggc aaa acc tta gtt ttt gaa caa aga aaa tca gat gga gtt cac act 464
 Gly Lys Thr Leu Val Phe Glu Gln Arg Lys Ser Asp Gly Val His Thr

35 85 90 95

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	gta gag act gaa gtt ggt gat tac atg ttc tgc ttt gac aat aca ttc	512
	Val Glu Thr Glu Val Gly Asp Tyr Met Phe Cys Phe Asp Asn Thr Phe	
	100 105 110	
5	agc acc att tct gag aag gtg att ttc ttt gaa tta atc ctg gat aat	560
	Ser Thr Ile Ser Glu Lys Val Ile Phe Phe Glu Leu Ile Leu Asp Asn	
	115 120 125	
	atg gga gaa cag gca caa gaa caa gaa gat tgg aag aaa tat att act	608
	Met Gly Glu Gln Ala Gln Glu Gln Glu Asp Trp Lys Lys Tyr Ile Thr	
	130 135 140	
10	ggc aca gat ata ttg gat atg aaa ctg gaa gac atc ctg gaa tcc atc	656
	Gly Thr Asp Ile Leu Asp Met Lys Leu Glu Asp Ile Leu Glu Ser Ile	
	145 150 155 160	
	aac agc atc aag tcc aga cta agc aaa agt ggg cac ata caa att ctg	704
	Asn Ser Ile Lys Ser Arg Leu Ser Lys Ser Gly His Ile Gln Ile Leu	
15	165 170 175	
	ctt aga gca ttt gaa gct cgt gat cga aac ata caa gaa agc aac ttt	752
	Leu Arg Ala Phe Glu Ala Arg Asp Arg Asn Ile Gln Glu Ser Asn Phe	
	180 185 190	
20	gat aga gtc aat ttc tgg tct atg gtt aat tta gtg gtc atg gtg gtg	800
	Asp Arg Val Asn Phe Trp Ser Met Val Asn Leu Val Val Met Val Val	
	195 200 205	
	gtg tca gcc att caa gtt tat atg ctg aag agt ctg ttt gaa gat aag	848
	Val Ser Ala Ile Gln Val Tyr Met Leu Lys Ser Leu Phe Glu Asp Lys	
	210 215 220	
25	agg aaa agt aga act taaaactcca aactagagta cgtaacattg aaaaatg	900
	Arg Lys Ser Arg Thr	
	225	
	aggcataaaaa atgcaataaaa ctgttacagt caagacc	937
30	<210> 53	
	<211> 1678	
	<212> DNA	
	<213> Homo sapiens	
	<220>	
35	<221> CDS	

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<222> (56)...(1459)

<400> 53

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5	atg cgg ccc cag gag ctc ccc agg ctc gcg ttc ccg ttg ctg ctg ttg	103
	Met Arg Pro Gln Glu Leu Pro Arg Leu Ala Phe Pro Leu Leu Leu Leu	
	1 5 10 15	
	ctg ttg ctg ctg ctg ccg ccg ccg ccg tgc cct gcc cac agc gcc acg	151
	Leu Leu Leu Leu Leu Pro Pro Pro Pro Cys Pro Ala His Ser Ala Thr	
10	20 25 30	
	cgc ttc gac ccc acc tgg gag tcc ctg gac gcc cgc cag ctg ccc gcg	199
	Arg Phe Asp Pro Thr Trp Glu Ser Leu Asp Ala Arg Gln Leu Pro Ala	
	35 40 45	
	tgg ttt gac cag gcc aag ttc ggc atc ttc atc cac tgg gga gtg ttt	247
15	Trp Phe Asp Gln Ala Lys Phe Gly Ile Phe Ile His Trp Gly Val Phe	
	50 55 60	
	tcc gtg ccc agc ttc ggt agc gag tgg ttc tgg tgg tat tgg caa aag	295
	Ser Val Pro Ser Phe Gly Ser Glu Trp Phe Trp Trp Tyr Trp Gln Lys	
	65 70 75 80	
20	gaa aag ata ccg aag tat gtg gaa ttt atg aaa gat aat tac cct cct	343
	Glu Lys Ile Pro Lys Tyr Val Glu Phe Met Lys Asp Asn Tyr Pro Pro	
	85 90 95	
	agt ttc aaa tat gaa gat ttt gga cca cta ttt aca gca aaa ttt ttt	391
	Ser Phe Lys Tyr Glu Asp Phe Gly Pro Leu Phe Thr Ala Lys Phe Phe	
25	100 105 110	
	aat gcc aac cag tgg gca gat att ttt cag gcc tct ggt gcc aaa tac	439
	Asn Ala Asn Gln Trp Ala Asp Ile Phe Gln Ala Ser Gly Ala Lys Tyr	
	115 120 125	
	att gtc tta act tcc aaa cat cat gaa ggc ttt acc ttg tgg ggg tca	487
30	Ile Val Leu Thr Ser Lys His His Glu Gly Phe Thr Leu Trp Gly Ser	
	130 135 140	
	gaa tat tcg tgg aac tgg aat gcc ata gat gag ggg ccc aag agg gac	535
	Glu Tyr Ser Trp Asn Trp Asn Ala Ile Asp Glu Gly Pro Lys Arg Asp	
	145 150 155 160	
35	att gtc aag gaa ctt gag gta gcc att agg aac aga act gac ctg cgt	583

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	Ile Val Lys Glu Leu Glu Val Ala Ile Arg Asn Arg Thr Asp Leu Arg	
	165 170 175	
	ttt gga ctg tac tat tcc ctt ttt gaa tgg ttt cat ccg ctc ttc ctt	631
	Phe Gly Leu Tyr Tyr Ser Leu Phe Glu Trp Phe His Pro Leu Phe Leu	
5	180 185 190	
	gag gat gaa tcc agt tca ttc cat aag cgg caa ttt cca gtt tct aag	679
	Glu Asp Glu Ser Ser Ser Phe His Lys Arg Gln Phe Pro Val Ser Lys	
	195 200 205	
	aca ttg cca gag ctc tat gag tta gtg aac aac tat cag cct gag gtt	727
10	Thr Leu Pro Glu Leu Tyr Glu Leu Val Asn Asn Tyr Gln Pro Glu Val	
	210 215 220	
	ctg tgg tcg gat ggt gac gga gga gca ccg gat caa tac tgg aac agc	775
	Leu Trp Ser Asp Gly Asp Gly Gly Ala Pro Asp Gln Tyr Trp Asn Ser	
	225 230 235 240	
15	aca ggc ttc ttg gcc tgg tta tat aat gaa agc cca gtt cgg ggc aca	823
	Thr Gly Phe Leu Ala Trp Leu Tyr Asn Glu Ser Pro Val Arg Gly Thr	
	245 250 255	
	gta gtc acc aat gat cgt tgg gga gct ggt agc atc tgt aag cat ggt	871
	Val Val Thr Asn Asp Arg Trp Gly Ala Gly Ser Ile Cys Lys His Gly	
20	260 265 270	
	ggc ttc tat acc tgc agt gat cgt tat aac cca gga cat ctt ttg cca	919
	Gly Phe Tyr Thr Cys Ser Asp Arg Tyr Asn Pro Gly His Leu Leu Pro	
	275 280 285	
	cat aaa tgg gaa aac tgc atg aca ata gac aaa ctg tcc tgg ggc tat	967
25	His Lys Trp Glu Asn Cys Met Thr Ile Asp Lys Leu Ser Trp Gly Tyr	
	290 295 300	
	agg agg gaa gct gga atc tct gac tat ctt aca att gaa gaa ttg gtg	1015
	Arg Arg Glu Ala Gly Ile Ser Asp Tyr Leu Thr Ile Glu Glu Leu Val	
	305 310 315 320	
30	aag caa ctt gta gag aca gtt tca tgt gga gga aat ctt ttg atg aat	1063
	Lys Gln Leu Val Glu Thr Val Ser Cys Gly Gly Asn Leu Leu Met Asn	
	325 330 335	
	att ggg ccc aca cta gat ggc acc att tct gta gtt ttt gag gag cga	1111
	Ile Gly Pro Thr Leu Asp Gly Thr Ile Ser Val Val Phe Glu Glu Arg	
35	340 345 350	

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	ctg agg caa atg ggg tcc tgg cta aaa gtc aat gga gaa gct att tat	1159
	Leu Arg Gln Met Gly Ser Trp Leu Lys Val Asn Gly Glu Ala Ile Tyr	
	355 360 365	
5	gaa acc cat acc tgg cga tcc cag aat gac act gtc acc cca gat gtg	1207
	Glu Thr His Thr Trp Arg Ser Gln Asn Asp Thr Val Thr Pro Asp Val	
	370 375 380	
	tgg tac aca tcc aag cct aaa gaa aaa tta gtc tat gcc att ttt ctt	1255
	Trp Tyr Thr Ser Lys Pro Lys Glu Lys Leu Val Tyr Ala Ile Phe Leu	
	385 390 395 400	
10	aaa tgg ccc aca tca gga cag ctg ttc ctt ggc cat ccc aaa gct att	1303
	Lys Trp Pro Thr Ser Gly Gln Leu Phe Leu Gly His Pro Lys Ala Ile	
	405 410 415	
	ctg ggg gca aca gag gtg aaa cta ctg ggc cat gga cag cca ctt aac	1351
	Leu Gly Ala Thr Glu Val Lys Leu Leu Gly His Gly Gln Pro Leu Asn	
15	420 425 430	
	tgg att tct ttg gag caa aat ggc att atg gta gaa ctg cca cag cta	1399
	Trp Ile Ser Leu Glu Gln Asn Gly Ile Met Val Glu Leu Pro Gln Leu	
	435 440 445	
	acc att cat cag atg ccg tgt aaa tgg ggc tgg gct cta gcc ctg act	1447
20	Thr Ile His Gln Met Pro Cys Lys Trp Gly Trp Ala Leu Ala Leu Thr	
	450 455 460	
	aat gtg atc taaagtgcag cagagtggct gatgctgcaa gttatgtcta aggc	1500
	Asn Val Ile	
	465	
25	taggaactat caggtgtcta taattgtagc acatggagaa agcaaagtga aaactggata	1560
	agaaaattat ttggcagtt cagcccttcc cctttttccc actaaatttt ttcttaaatt	1620
	acccatgtaa ccattttaac totccagtgc actttgccat taaagtctct tcacattg	1678
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5

Met

1

gat aac gtg cag ccg aaa ata aaa cat cgc ccc ttc tgc ttc agt gtg 164
 Asp Asn Val Gln Pro Lys Ile Lys His Arg Pro Phe Cys Phe Ser Val

5

10

15

10 aaa ggc cac gtg aag atg ctg cgg ctg gat att atc aac tca ctg gta 212
 Lys Gly His Val Lys Met Leu Arg Leu Asp Ile Ile Asn Ser Leu Val

20

25

30

aca aca gta ttc atg ctc atc gta tct gtg ttg gca ctg ata cca gaa 260
 Thr Thr Val Phe Met Leu Ile Val Ser Val Leu Ala Leu Ile Pro Glu

15

35

40

45

acc aca aca ttg aca gtt ggt gga ggg gtg ttt gca ctt gtg aca gca 308
 Thr Thr Thr Leu Thr Val Gly Gly Gly Val Phe Ala Leu Val Thr Ala

50

55

60

65

gta tgc tgt ctt gcc gac ggg gcc ctt att tac cgg aag ctt ctg ttc 356
 Val Cys Cys Leu Ala Asp Gly Ala Leu Ile Tyr Arg Lys Leu Leu Phe

20

70

75

80

aat ccc agc ggt cct tac cag caa aag cct gtg cat gaa aaa aaa gaa 404
 Asn Pro Ser Gly Pro Tyr Gln Gln Lys Pro Val His Glu Lys Lys Glu

85

90

95

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catattttctg tattctt

467

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	gggtgctgcg gattgaggtc ccggttccta acgaatctct gctggattgg ccgtaaccct	180
	gtccccgagc gggctcacag ggtctgaagg ccacgcatga ggcaaaggta aagttctgag	240
	ccaccgggtg cctccttccc aggactgcaa g atg gag gaa ggc ggg aac cta	292
	Met Glu Glu Gly Gly Asn Leu	
10	1 5	
	gga ggc ctg att aag atg gtc cat cta ctg gtc ttg tca ggt gcc tgg	340
	Gly Gly Leu Ile Lys Met Val His Leu Leu Val Leu Ser Gly Ala Trp	
	10 15 20	
	ggc atg caa atg tgg gtg acc ttc gtc tca ggc ttc ctg ctt ttc cga	388
15	Gly Met Gln Met Trp Val Thr Phe Val Ser Gly Phe Leu Leu Phe Arg	
	25 30 35	
	agc ctt ccc cga cat acc ttc gga cta gtg cag agc aaa ctc ttc ccc	436
	Ser Leu Pro Arg His Thr Phe Gly Leu Val Gln Ser Lys Leu Phe Pro	
	40 45 50 55	
20	ttc tac ttc cac atc tcc atg ggc tgt gcc ttc atc aac ctc tgc atc	484
	Phe Tyr Phe His Ile Ser Met Gly Cys Ala Phe Ile Asn Leu Cys Ile	
	60 65 70	
	ttg gct tca cag cat gct tgg gct cag ctc aca ttc tgg gag gcc agc	532
	Leu Ala Ser Gln His Ala Trp Ala Gln Leu Thr Phe Trp Glu Ala Ser	
25	75 80 85	
	cag ctt tac ctg ctg ttc ctg agc ctt acg ctg gcc act gtc aac gcc	580
	Gln Leu Tyr Leu Leu Phe Leu Ser Leu Thr Leu Ala Thr Val Asn Ala	
	90 95 100	
	cgc tgg ctg gaa ccc cgc acc aca gct gcc atg tgg gcc ctg caa acc	628
30	Arg Trp Leu Glu Pro Arg Thr Thr Ala Ala Met Trp Ala Leu Gln Thr	
	105 110 115	
	gtg gag aag gag cga ggc ctg ggt ggg gag gta cca ggc agc cac cag	676
	Val Glu Lys Glu Arg Gly Leu Gly Gly Glu Val Pro Gly Ser His Gln	
	120 125 130 135	
35	ggt ccc gat ccc tac cgc cag ctg cga gag aag gac ccc aag tac agt	724

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Gly Pro Asp Pro Tyr Arg Gln Leu Arg Glu Lys Asp Pro Lys Tyr Ser
 140 145 150
 gct ctc cgc cag aat ttc ttc cgc tac cat ggg ctg tcc tct ctt tgc 772
 Ala Leu Arg Gln Asn Phe Phe Arg Tyr His Gly Leu Ser Ser Leu Cys
 5 155 160 165
 aat ctg ggc tgc gtc ctg agc aat ggg ctc tgt ctc gct ggc ctt gcc 820
 Asn Leu Gly Cys Val Leu Ser Asn Gly Leu Cys Leu Ala Gly Leu Ala
 170 175 180
 ctg gaa ata agg agc ctc tagcatgggc cctgcatgct aataaatgct tcttcag 875
 10 Leu Glu Ile Arg Ser Leu
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 cagatgccaa agccaagtcc ccaccgacc atg gtg gac agc ctc ctg gca gtc 173
 25 Met Val Asp Ser Leu Leu Ala Val
 1 5
 acc ctg gct gga aac ctg ggc ctg acc ttc ctc cga ggt tcc cag acc 221
 Thr Leu Ala Gly Asn Leu Gly Leu Thr Phe Leu Arg Gly Ser Gln Thr
 10 15 20
 30 cag agc cat cca gac ctg gga act gag ggc tgc tgg gac cag ctc tct 269
 Gln Ser His Pro Asp Leu Gly Thr Glu Gly Cys Trp Asp Gln Leu Ser
 25 30 35 40
 gcc cct cgg acc ttt acg ctt ttg gac ccc aag gca tct ctg tta acc 317
 Ala Pro Arg Thr Phe Thr Leu Leu Asp Pro Lys Ala Ser Leu Leu Thr
 35 45 50 55

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	aag gcc ttc ctc aat ggc gcc ctg gat ggg gtc atc ctt gga gac tac	365
	Lys Ala Phe Leu Asn Gly Ala Leu Asp Gly Val Ile Leu Gly Asp Tyr	
	60 65 70	
	ctg agc cgg act cct gag ccc cgg cca tcc ctc agc cac ttg ctg agc	413
5	Leu Ser Arg Thr Pro Glu Pro Arg Pro Ser Leu Ser His Leu Leu Ser	
	75 80 85	
	cag tac tat ggg gct ggg gtg gcc aga gac cca ggg ttc cgc agc aac	461
	Gln Tyr Tyr Gly Ala Gly Val Ala Arg Asp Pro Gly Phe Arg Ser Asn	
	90 95 100	
10	ttc cga cgg cag aac ggt gct gct ctg act tca gcc tcc atc ctg gcc	509
	Phe Arg Arg Gln Asn Gly Ala Ala Leu Thr Ser Ala Ser Ile Leu Ala	
	105 110 115 120	
	cag cag gtg tgg gga acc ctt gtc ctt cta cag agg ctg gag cca gta	557
	Gln Gln Val Trp Gly Thr Leu Val Leu Leu Gln Arg Leu Glu Pro Val	
15	125 130 135	
	cac ctc cag ctt cag tgc atg agc caa gaa cag ctg gcc cag gtg gct	605
	His Leu Gln Leu Gln Cys Met Ser Gln Glu Gln Leu Ala Gln Val Ala	
	140 145 150	
	gcc aat gct acc aag gaa ttc act gag gcc ttc ctg gga tgc ccg gcc	653
20	Ala Asn Ala Thr Lys Glu Phe Thr Glu Ala Phe Leu Gly Cys Pro Ala	
	155 160 165	
	atc cac ccc cgc tgc cgc tgg gga gcg gcg cct tat cgg ggc cgc ccg	701
	Ile His Pro Arg Cys Arg Trp Gly Ala Ala Pro Tyr Arg Gly Arg Pro	
	170 175 180	
25	aag ctg ctg cag ctg ccg ctg gga ttc ttg tac gtg cat cac acc tac	749
	Lys Leu Leu Gln Leu Pro Leu Gly Phe Leu Tyr Val His His Thr Tyr	
	185 190 195 200	
	gtg cct gca cca ccc tgc acg gac ttc acg cgc tgc gca gcc aac atg	797
	Val Pro Ala Pro Pro Cys Thr Asp Phe Thr Arg Cys Ala Ala Asn Met	
30	205 210 215	
	cgc tcc atg cag cgc tac cac cag gac acg caa ggc tgg gga gac atc	845
	Arg Ser Met Gln Arg Tyr His Gln Asp Thr Gln Gly Trp Gly Asp Ile	
	220 225 230	
	ggc tac agt ttc gtg gtg ggc tcg gac ggc tac gtg tac gag gga cgc	893
35	Gly Tyr Ser Phe Val Val Gly Ser Asp Gly Tyr Val Tyr Glu Gly Arg	

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	235	240	245	
	ggc tgg cac tgg gtg ggc gcc cac acg ctc ggc cac aac tcc cgg ggc			941
	Gly Trp His Trp Val Gly Ala His Thr Leu Gly His Asn Ser Arg Gly			
	250	255	260	
5	ttc ggc gtg gcc ata gtg ggc aac tac acc gcg gcg ctg ccc acc gag			989
	Phe Gly Val Ala Ile Val Gly Asn Tyr Thr Ala Ala Leu Pro Thr Glu			
	265	270	275	280
	gcc gct ctg cgc acg gtg cgc gac acg ctc ccg agt tgt gcg gtg cgc			1037
	Ala Ala Leu Arg Thr Val Arg Asp Thr Leu Pro Ser Cys Ala Val Arg			
10		285	290	295
	gcc ggc ctc ctg cgg cca gac tac gcg ctg ctg ggc cac cgc cag ctg			1085
	Ala Gly Leu Leu Arg Pro Asp Tyr Ala Leu Leu Gly His Arg Gln Leu			
	300	305	310	
	gtg cgc acc gac tgc ccc ggc gac gcg ctc ttc gac ctg ctg cgc acc			1133
15	Val Arg Thr Asp Cys Pro Gly Asp Ala Leu Phe Asp Leu Leu Arg Thr			
	315	320	325	
	tgg ccg cac ttc acc gcg act gtt aag cca aga cct gcc agg agt gtc			1181
	Trp Pro His Phe Thr Ala Thr Val Lys Pro Arg Pro Ala Arg Ser Val			
	330	335	340	
20	tct aag aga tcc agg agg gag cca ccc cca agg acc ctg cca gcc aca			1229
	Ser Lys Arg Ser Arg Arg Glu Pro Pro Pro Arg Thr Leu Pro Ala Thr			
	345	350	355	360
	gac ctc caa taaagacagc atggaaac			1256
	Asp Leu Gln			
25				
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	gctggagacc tccgcgtgg ccccccgcgag cctcctgccc tggcccggcg ctgaggctct	120
	gccgcggcgg cagc atg ggt ggc ccc cgg ggc gcg ggc tgg gtg gcg gcg	170
	Met Gly Gly Pro Arg Gly Ala Gly Trp Val Ala Ala	
	1 5 10	
5	ggc ctg ctg ctc ggc gcg ggc gcc tgc tac tgc att tac agg ctg acc	218
	Gly Leu Leu Leu Gly Ala Gly Ala Cys Tyr Cys Ile Tyr Arg Leu Thr	
	15 20 25	
	cgg ggt cgg cgg cgg ggc gac cgc gag ctc ggg ata cgc tct tcg aag	266
	Arg Gly Arg Arg Arg Gly Asp Arg Glu Leu Gly Ile Arg Ser Ser Lys	
10	30 35 40	
	tcc gca gaa gac tta act gat ggt tca tat gat gat gtt cta aat gct	314
	Ser Ala Glu Asp Leu Thr Asp Gly Ser Tyr Asp Asp Val Leu Asn Ala	
	45 50 55 60	
	gaa caa ctt cag aaa ctc ctt tac ctg ctg gag tca acg gag gat cct	362
15	Glu Gln Leu Gln Lys Leu Leu Tyr Leu Leu Glu Ser Thr Glu Asp Pro	
	65 70 75	
	gta att att gaa aga gct ttg att act ttg ggt aac aat gca gcc ttt	410
	Val Ile Ile Glu Arg Ala Leu Ile Thr Leu Gly Asn Asn Ala Ala Phe	
	80 85 90	
20	tca gtt aac caa gct att att cgt gaa ttg ggt ggt att cca att gtt	458
	Ser Val Asn Gln Ala Ile Ile Arg Glu Leu Gly Gly Ile Pro Ile Val	
	95 100 105	
	gca aac aaa atc aac cat tcc aac cag agt att aaa gag aaa gct tta	506
	Ala Asn Lys Ile Asn His Ser Asn Gln Ser Ile Lys Glu Lys Ala Leu	
25	110 115 120	
	aat gca cta aat aac ctg agt gtg aat gtt gaa aat caa atc aag ata	554
	Asn Ala Leu Asn Asn Leu Ser Val Asn Val Glu Asn Gln Ile Lys Ile	
	125 130 135 140	
	aag gtg caa gtt ttg aaa ctg ctt ttg aat ttg tct gaa aat cca gcc	602
30	Lys Val Gln Val Leu Lys Leu Leu Leu Asn Leu Ser Glu Asn Pro Ala	
	145 150 155	
	atg aca gaa gga ctt ctc cgt gcc caa gtg gat tca tca ttc ctt tcc	650
	Met Thr Glu Gly Leu Leu Arg Ala Gln Val Asp Ser Ser Phe Leu Ser	
	160 165 170	
35	ctt tat gac agc cac gta gca aag gag att ctt ctt cga gta ctt acg	698

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Leu Tyr Asp Ser His Val Ala Lys Glu Ile Leu Leu Arg Val Leu Thr
 175 180 185
 cta ttt cag aat ata aag aac tgc ctc aaa ata gaa ggc cat tta gct 746
 Leu Phe Gln Asn Ile Lys Asn Cys Leu Lys Ile Glu Gly His Leu Ala
 5 190 195 200
 gtg cag cct act ttc act gaa ggt tca ttg ttt ttc ctg tta cat gga 794
 Val Gln Pro Thr Phe Thr Glu Gly Ser Leu Phe Phe Leu Leu His Gly
 205 210 215 220
 gaa gaa tgt gcc cag aaa ata aga gct tta gtt gat cac cat gat gca 842
 10 Glu Glu Cys Ala Gln Lys Ile Arg Ala Leu Val Asp His His Asp Ala
 225 230 235
 gag gtg aag gaa aag gtt gta aca ata ata ccc aaa atc tga 884
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 Leu Leu Cys Cys Gly Pro Lys Leu Ala Ala Cys Gly Ile Val Leu Ser
 30 5 10 15
 gcc tgg gga gtg atc atg ttg ata atg ctc gga ata ttt ttc aat gtc 152
 Ala Trp Gly Val Ile Met Leu Ile Met Leu Gly Ile Phe Phe Asn Val
 20 25 30 35
 cat tcc gct gtg ttg att gag gac gtt ccc ttc acg gag aaa gat ttt 200
 35 His Ser Ala Val Leu Ile Glu Asp Val Pro Phe Thr Glu Lys Asp Phe

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	40	45	50	
	gag aat ggc ccc cag aac ata tac aac ctt tac gag caa gtc agc tac			248
	Glu Asn Gly Pro Gln Asn Ile Tyr Asn Leu Tyr Glu Gln Val Ser Tyr			
	55	60	65	
5	aac tgt ttc atc gct gca ggc ctt tac ctc ctc ctc gga ggc ttc tct			296
	Asn Cys Phe Ile Ala Ala Gly Leu Tyr Leu Leu Leu Gly Gly Phe Ser			
	70	75	80	
	ttc tgc caa gtt cgg ctc aat aag cgc aag gaa tac atg gtg cgc			341
	Phe Cys Gln Val Arg Leu Asn Lys Arg Lys Glu Tyr Met Val Arg			
10	85	90	95	
	tagggcccc ggcgcgtttc cccgctccag cccctcctct atttaaagac tccctgcacc			400
	gtgtcacecca ggtegcgtcc cacccttgcc ggcgcctct gtgggactgg gtttcccg			460
	cgagagactg aatcccttct cccatctctg gcatecggcc cccgtggaga gggctgaggc			520
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	1	5		
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30	Leu Arg Pro Leu Ala Ala Leu Ala Leu Val Leu Ala Leu Ala Pro Gly			
	10	15	20	25
	ctg ccc aca gcc cgg gcc ggg cag aca ccg cgc cct gcc gag cgg ggg			147
	Leu Pro Thr Ala Arg Ala Gly Gln Thr Pro Arg Pro Ala Glu Arg Gly			
	30	35	40	
35	ccc cca gtg cgg ctt ttc acc gag gag gag ctg gcc cgc tat ggc ggg			195

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	Pro Pro Val Arg Leu Phe Thr Glu Glu Glu Leu Ala Arg Tyr Gly Gly	
	45 50 55	
	gag gag gaa gat cag ccc atc tac ttg gca gtg aag gga gtg gtg ttt	243
	Glu Glu Glu Asp Gln Pro Ile Tyr Leu Ala Val Lys Gly Val Val Phe	
5	60 65 70	
	gat gtc acc tcc gga aag gag ttt tat gga cga gga gcc ccc tac aat	291
	Asp Val Thr Ser Gly Lys Glu Phe Tyr Gly Arg Gly Ala Pro Tyr Asn	
	75 80 85	
	gcc ttg acg ggg aag gac tcc act aga ggg gta gcc aag atg tcc ttg	339
10	Ala Leu Thr Gly Lys Asp Ser Thr Arg Gly Val Ala Lys Met Ser Leu	
	90 95 100 105	
	gat cct gca gac ctc acc cat gac act acg ggt ctc acg gcc aag gaa	387
	Asp Pro Ala Asp Leu Thr His Asp Thr Thr Gly Leu Thr Ala Lys Glu	
	110 115 120	
15	ctg gag gcc ctg gat gag gtc ttc acc aaa gtg tac aaa gcc aaa tac	435
	Leu Glu Ala Leu Asp Glu Val Phe Thr Lys Val Tyr Lys Ala Lys Tyr	
	125 130 135	
	ccc atc gtc ggc tac act gcc cgg aga att ctc aat gag gat ggc agc	483
	Pro Ile Val Gly Tyr Thr Ala Arg Arg Ile Leu Asn Glu Asp Gly Ser	
20	140 145 150	
	cct aac ctg gac ttc aag cct gaa gac cag ccc cat ttt gac atc aag	531
	Pro Asn Leu Asp Phe Lys Pro Glu Asp Gln Pro His Phe Asp Ile Lys	
	155 160 165	
	gat gag ttc tgatgttccc cctgcaggag caggttcttg ggagcgtgag	580
25	Asp Glu Phe	
	170	
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	cgtgtt atg atg ccg tcc cgt acc aac ctg gct act gga atc ccc agt	168
	Met Met Pro Ser Arg Thr Asn Leu Ala Thr Gly Ile Pro Ser	
	1 5 10	
	agt aaa gtg aaa tat tca agg ctc tcc agc aca gac gat ggc tac att	216
10	Ser Lys Val Lys Tyr Ser Arg Leu Ser Ser Thr Asp Asp Gly Tyr Ile	
	15 20 25 30	
	gac ctt cag ttt aag aaa acc cct cct aag atc cct tat aag gcc atc	264
	Asp Leu Gln Phe Lys Lys Thr Pro Pro Lys Ile Pro Tyr Lys Ala Ile	
	35 40 45	
15	gca ctt gcc act gtg ctg ttt ttg att ggc gcc ttt ctc att att ata	312
	Ala Leu Ala Thr Val Leu Phe Leu Ile Gly Ala Phe Leu Ile Ile Ile	
	50 55 60	
	ggc tcc ctc ctg ctg tca ggc tac atc agc aaa ggg ggg gca gac cgg	360
	Gly Ser Leu Leu Leu Ser Gly Tyr Ile Ser Lys Gly Gly Ala Asp Arg	
20	65 70 75	
	gcc gtt cca gtg ctg atc att ggc att ctg gtg ttc cta ccc gga ttt	408
	Ala Val Pro Val Leu Ile Ile Gly Ile Leu Val Phe Leu Pro Gly Phe	
	80 85 90	
	tac cac ctg cgc atc gct tac tat gca tcc aaa ggc tac cgt ggt tac	456
25	Tyr His Leu Arg Ile Ala Tyr Tyr Ala Ser Lys Gly Tyr Arg Gly Tyr	
	95 100 105 110	
	tcc tat gat gac att cca gac ttt gat gac tagcaccac ccca	500
	Ser Tyr Asp Asp Ile Pro Asp Phe Asp Asp	
	115 120	
30	tagctgagga ggagtcacag tggaactgtc ccagctttaa gatattctagc agaaactata	560
	gctgaggact aaggaattct gcagcttgca gatgtttaaag aaaataatgg ccagattttt	620
	tgggtccttc ccaaagatgt taagtgaacc tacagttagc taattaggac aagctctatt	680
	tttcatccct gggccctgac aagtttttcc acaggaatat gtatcatgga agaatagagg	740
	ttattctgta atggaaaagt gttgcctgcc accacctct gtagagctga gcatttcttt	800
35	taaatagtct tcattgccaa tttgttcttg tagcaaatgg aacaatgtgg tatggcta	860

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<211> 307

<212> PRT

15 <213> Homo sapiens

<400> 61

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 20 Pro Leu Ser Ala Ser Thr Asp Tyr Glu Gln Ser Thr Gly Met Gln Glu
 20 25 30
 Cys Arg Lys Tyr Phe Lys Met Leu Ser Arg Lys Leu Ala Gln Leu Pro
 35 40 45
 Asp Arg Cys Thr Leu Lys Thr Gly His Tyr Asn Ile Asn Phe Ile Ser
 25 50 55 60
 Ser Leu Gly Val Ser Tyr Met Met Leu Cys Thr Glu Asn Tyr Pro Asn
 65 70 75 80
 Val Leu Ala Phe Ser Phe Leu Asp Glu Leu Gln Lys Glu Phe Ile Thr
 85 90 95
 30 Thr Tyr Asn Met Met Lys Thr Asn Thr Ala Val Arg Pro Tyr Cys Phe
 100 105 110
 Ile Glu Phe Asp Asn Phe Ile Gln Arg Thr Lys Gln Arg Tyr Asn Asn
 115 120 125
 Pro Arg Ser Leu Ser Thr Lys Ile Asn Leu Ser Asp Met Gln Thr Glu
 35 130 135 140

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Ile Lys Leu Arg Pro Pro Tyr Gln Ile Ser Met Cys Glu Leu Gly Ser
 145 150 155 160
 Ala Asn Gly Val Thr Ser Ala Phe Ser Val Asp Cys Lys Gly Ala Gly
 165 170 175
 5 Lys Ile Ser Ser Ala His Gln Arg Leu Glu Pro Ala Thr Leu Ser Gly
 180 185 190
 Ile Val Gly Phe Ile Leu Ser Leu Leu Cys Gly Ala Leu Asn Leu Ile
 195 200 205
 Arg Gly Phe His Ala Ile Glu Ser Leu Leu Gln Ser Asp Gly Asp Asp
 10 210 215 220
 Phe Asn Tyr Ile Ile Ala Phe Phe Leu Gly Thr Ala Ala Cys Leu Tyr
 225 230 235 240
 Gln Cys Tyr Leu Leu Val Tyr Tyr Thr Gly Trp Arg Asn Val Lys Ser
 245 250 255
 15 Phe Leu Thr Phe Gly Leu Ile Cys Leu Cys Asn Met Tyr Leu Tyr Glu
 260 265 270
 Leu Arg Asn Leu Trp Gln Leu Phe Phe His Val Thr Val Gly Ala Phe
 275 280 285
 Val Thr Leu Gln Ile Trp Leu Arg Gln Ala Gln Gly Lys Ala Pro Asp
 20 290 295 300
 Tyr Asp Val
 305

 <210> 62
 25 <211> 183
 <212> PRT
 <213> Homo sapiens

 <400> 62
 30 Met Thr Ala Gln Gly Gly Leu Val Ala Asn Arg Gly Arg Arg Phe Lys
 1 5 10 15
 Trp Ala Ile Glu Leu Ser Gly Pro Gly Gly Gly Ser Arg Gly Arg Ser
 20 25 30
 Asp Arg Gly Ser Gly Gln Gly Asp Ser Leu Tyr Pro Val Gly Tyr Leu
 35 35 40 45

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Asp Lys Gln Val Pro Asp Thr Ser Val Gln Glu Thr Asp Arg Ile Leu
 50 55 60
 Val Glu Lys Arg Cys Trp Asp Ile Ala Leu Gly Pro Leu Lys Gln Ile
 65 70 75 80
 5 Pro Met Asn Leu Phe Ile Met Tyr Met Ala Gly Asn Thr Ile Ser Ile
 85 90 95
 Phe Pro Thr Met Met Val Cys Met Met Ala Trp Arg Pro Ile Gln Ala
 100 105 110
 Leu Met Ala Ile Ser Ala Thr Phe Lys Met Leu Glu Ser Ser Ser Gln
 10 115 120 125
 Lys Phe Leu Gln Gly Leu Val Tyr Leu Ile Gly Asn Leu Met Gly Leu
 130 135 140
 Ala Leu Ala Val Tyr Lys Cys Gln Ser Met Gly Leu Leu Pro Thr His
 145 150 155 160
 15 Ala Ser Asp Trp Leu Ala Phe Ile Glu Pro Pro Glu Arg Met Glu Phe
 165 170 175
 Ser Gly Gly Gly Leu Leu Leu
 180
 20 <210> 63
 <211> 327
 <212> PRT
 <213> Homo sapiens
 25 <400> 63
 Met Arg Ala Leu Pro Gly Leu Leu Glu Ala Arg Ala Arg Thr Pro Arg
 1 5 10 15
 Leu Leu Leu Leu Gln Cys Leu Leu Ala Ala Ala Arg Pro Ser Ser Ala
 20 25 30
 30 Asp Gly Ser Ala Pro Asp Ser Pro Phe Thr Ser Pro Pro Leu Arg Glu
 35 40 45
 Glu Ile Met Ala Asn Asn Phe Ser Leu Glu Ser His Asn Ile Ser Leu
 50 55 60
 Thr Glu His Ser Ser Met Pro Val Glu Lys Asn Ile Thr Leu Glu Arg
 35 65 70 75 80

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Pro Ser Asn Val Asn Leu Thr Cys Gln Phe Thr Thr Ser Gly Asp Leu
 85 90 95
 Asn Ala Val Asn Val Thr Trp Lys Lys Asp Gly Glu Gln Leu Glu Asn
 100 105 110
 5 Asn Tyr Leu Val Ser Ala Thr Gly Ser Thr Leu Tyr Thr Gln Tyr Arg
 115 120 125
 Phe Thr Ile Ile Asn Ser Lys Gln Met Gly Ser Tyr Ser Cys Phe Phe
 130 135 140
 Arg Glu Glu Lys Glu Gln Arg Gly Thr Phe Asn Phe Lys Val Pro Glu
 10 145 150 155 160
 Leu His Gly Lys Asn Lys Pro Leu Ile Ser Tyr Val Gly Asp Ser Thr
 165 170 175
 Val Leu Thr Cys Lys Cys Gln Asn Cys Phe Pro Leu Asn Trp Thr Trp
 180 185 190
 15 Tyr Ser Ser Asn Gly Ser Val Lys Val Pro Val Gly Val Gln Met Asn
 195 200 205
 Lys Tyr Val Ile Asn Gly Thr Tyr Ala Asn Glu Thr Lys Leu Lys Ile
 210 215 220
 Thr Gln Leu Leu Glu Glu Asp Gly Glu Ser Tyr Trp Cys Arg Ala Leu
 20 225 230 235 240
 Phe Gln Leu Gly Glu Ser Glu Glu His Ile Glu Leu Val Val Leu Ser
 245 250 255
 Tyr Leu Val Pro Leu Lys Pro Phe Leu Val Ile Val Ala Glu Val Ile
 260 265 270
 25 Leu Leu Val Ala Thr Ile Leu Leu Cys Glu Lys Tyr Thr Gln Lys Lys
 275 280 285
 Lys Lys His Ser Asp Glu Gly Lys Glu Phe Glu Gln Ile Glu Gln Leu
 290 295 300
 Lys Ser Asp Asp Ser Asn Gly Ile Glu Asn Asn Val Pro Arg His Arg
 30 305 310 315 320
 Lys Asn Glu Ser Leu Gly Gln
 325

<210> 64

35 <211> 223

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<212> PRT

<213> Homo sapiens

<400> 64

5 Met Lys Phe Val Pro Cys Leu Leu Leu Val Thr Leu Ser Cys Leu Gly
 1 5 10 15
 Thr Leu Gly Gln Ala Pro Arg Gln Lys Gln Gly Ser Thr Gly Glu Glu
 20 25 30
 Phe His Phe Gln Thr Gly Gly Arg Asp Ser Cys Thr Met Arg Pro Ser
 10 35 40 45
 Ser Leu Gly Gln Gly Ala Gly Glu Val Trp Leu Arg Val Asp Cys Arg
 50 55 60
 Asn Thr Asp Gln Thr Tyr Trp Cys Glu Tyr Arg Gly Gln Pro Ser Met
 65 70 75 80
 15 Cys Gln Ala Phe Ala Ala Asp Pro Lys Ser Tyr Trp Asn Gln Ala Leu
 85 90 95
 Gln Glu Leu Arg Arg Leu His His Ala Cys Gln Gly Ala Pro Val Leu
 100 105 110
 Arg Pro Ser Val Cys Arg Glu Ala Gly Pro Gln Ala His Met Gln Gln
 20 115 120 125
 Val Thr Ser Ser Leu Lys Gly Ser Pro Glu Pro Asn Gln Gln Pro Glu
 130 135 140
 Ala Gly Thr Pro Ser Leu Arg Pro Lys Ala Thr Val Lys Leu Thr Glu
 145 150 155 160
 25 Ala Thr Gln Leu Gly Lys Asp Ser Met Glu Glu Leu Gly Lys Ala Lys
 165 170 175
 Pro Thr Thr Arg Pro Thr Ala Lys Pro Thr Gln Pro Gly Pro Arg Pro
 180 185 190
 Gly Gly Asn Glu Glu Ala Lys Lys Lys Ala Trp Glu His Cys Trp Lys
 30 195 200 205
 Pro Phe Gln Ala Leu Cys Ala Phe Leu Ile Ser Phe Phe Arg Gly
 210 215 220

<210> 65

35 <211> 48

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<212> PRT

<213> Homo sapiens

<400> 65

5 Met Arg Leu Leu Leu Leu Leu Val Ala Ala Ser Ala Met Val Arg
 1 5 10 15
 Ser Glu Ala Ser Ala Asn Leu Gly Gly Val Pro Ser Lys Arg Leu Lys
 20 25 30
 10 Met Gln Tyr Ala Thr Gly Pro Leu Leu Lys Phe Gln Ile Cys Val Ser
 35 40 45

<210> 66

<211> 371

<212> PRT

15 <213> Homo sapiens

<400> 66

Met Ala Trp Thr Lys Tyr Gln Leu Phe Leu Ala Gly Leu Met Leu Val
 1 5 10 15
 20 Thr Gly Ser Ile Asn Thr Leu Ser Ala Lys Trp Ala Asp Asn Phe Met
 20 25 30
 Ala Glu Gly Cys Gly Gly Ser Lys Glu His Ser Phe Gln His Pro Phe
 35 40 45
 Leu Gln Ala Val Gly Met Phe Leu Gly Glu Phe Ser Cys Leu Ala Ala
 25 50 55 60
 Phe Tyr Leu Leu Arg Cys Arg Ala Ala Gly Gln Ser Asp Ser Ser Val
 65 70 75 80
 Asp Pro Gln Gln Pro Phe Asn Pro Leu Leu Phe Leu Pro Pro Ala Leu
 85 90 95
 30 Cys Asp Met Thr Gly Thr Ser Leu Met Tyr Val Ala Leu Asn Met Thr
 100 105 110
 Ser Ala Ser Ser Phe Gln Met Leu Arg Gly Ala Val Ile Ile Phe Thr
 115 120 125
 Gly Leu Phe Ser Val Ala Phe Leu Gly Arg Arg Leu Val Leu Ser Gln
 35 130 135 140

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Trp Leu Gly Ile Leu Ala Thr Ile Ala Gly Leu Val Val Val Gly Leu
 145 150 155 160
 Ala Asp Leu Leu Ser Lys His Asp Ser Gln His Lys Leu Ser Glu Val
 165 170 175
 5 Ile Thr Gly Asp Leu Leu Ile Ile Met Ala Gln Ile Ile Val Ala Ile
 180 185 190
 Gln Met Val Leu Glu Glu Lys Phe Val Tyr Lys His Asn Val His Pro
 195 200 205
 10 Leu Arg Ala Val Gly Thr Glu Gly Leu Phe Gly Phe Val Ile Leu Ser
 210 215 220
 Leu Leu Leu Val Pro Met Tyr Tyr Ile Pro Ala Gly Ser Phe Ser Gly
 225 230 235 240
 Asn Pro Arg Gly Thr Leu Glu Asp Ala Leu Asp Ala Phe Cys Gln Val
 245 250 255
 15 Gly Gln Gln Pro Leu Ile Ala Val Ala Leu Leu Gly Asn Ile Ser Ser
 260 265 270
 Ile Ala Phe Phe Asn Phe Ala Gly Ile Ser Val Thr Lys Glu Leu Ser
 275 280 285
 20 Ala Thr Thr Arg Met Val Leu Asp Ser Leu Arg Thr Val Val Ile Trp
 290 295 300
 Ala Leu Ser Leu Ala Leu Gly Trp Glu Ala Phe His Ala Leu Gln Ile
 305 310 315 320
 Leu Gly Phe Leu Ile Leu Leu Ile Gly Thr Ala Leu Tyr Asn Gly Leu
 325 330 335
 25 His Arg Pro Leu Leu Gly Arg Leu Ser Arg Gly Arg Pro Leu Ala Glu
 340 345 350
 Glu Ser Glu Gln Glu Arg Leu Leu Gly Gly Thr Arg Thr Pro Ile Asn
 355 360 365
 Asp Ala Ser
 30 370

 <210> 67
 <211> 90
 <212> PRT
 35 <213> Homo sapiens

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<400> 67

Met Phe His Gln Ile Trp Ala Ala Leu Leu Tyr Phe Tyr Gly Ile Ile
 1 5 10 15
 5 Leu Asn Ser Ile Tyr Gln Cys Pro Glu His Ser Gln Leu Thr Thr Leu
 20 25 30
 Gly Val Asp Gly Lys Glu Phe Pro Glu Val His Leu Gly Gln Trp Tyr
 35 40 45
 Phe Ile Ala Gly Ala Ala Pro Thr Lys Glu Glu Leu Ala Thr Phe Asp
 10 50 55 60
 Pro Val Asp Asn Ile Val Phe Asn Met Ala Ala Gly Ser Ala Pro Met
 65 70 75 80
 Gln Leu His Leu Arg Ala Thr Ile Arg Met
 85 90

15

<210> 68

<211> 499

<212> PRT

<213> Homo sapiens

20

<400> 68

Met Val Asp Arg Gly Pro Leu Leu Thr Ser Ala Ile Ile Phe Tyr Leu
 1 5 10 15
 Ala Ile Gly Ala Ala Ile Phe Glu Val Leu Glu Glu Pro His Trp Lys
 25 20 25 30
 Glu Ala Lys Lys Asn Tyr Tyr Thr Gln Lys Leu His Leu Leu Lys Glu
 35 40 45
 Phe Pro Cys Leu Gly Gln Glu Gly Leu Asp Lys Ile Leu Glu Val Val
 50 55 60
 30 Ser Asp Ala Ala Gly Gln Gly Val Ala Ile Thr Gly Asn Gln Thr Phe
 65 70 75 80
 Asn Asn Trp Asn Trp Pro Asn Ala Met Ile Phe Ala Ala Thr Val Ile
 85 90 95
 Thr Thr Ile Gly Tyr Gly Asn Val Ala Pro Lys Thr Pro Ala Gly Arg
 35 100 105 110

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Leu Phe Cys Val Phe Tyr Gly Leu Phe Gly Val Pro Leu Cys Leu Thr
 115 120 125
 Trp Ile Ser Ala Leu Gly Lys Phe Phe Gly Gly Arg Ala Lys Arg Leu
 130 135 140
 5 Gly Gln Phe Leu Thr Lys Arg Gly Val Ser Leu Arg Lys Ala Gln Ile
 145 150 155 160
 Thr Cys Thr Val Ile Phe Ile Val Trp Gly Val Leu Val His Leu Val
 165 170 175
 Ile Pro Pro Phe Val Phe Met Val Thr Glu Gly Trp Asn Tyr Ile Glu
 10 180 185 190
 Gly Leu Tyr Tyr Ser Phe Ile Thr Ile Ser Thr Ile Gly Phe Gly Asp
 195 200 205
 Phe Val Ala Gly Val Asn Pro Ser Ala Asn Tyr His Ala Leu Tyr Arg
 210 215 220
 15 Tyr Phe Val Glu Leu Trp Ile Tyr Leu Gly Leu Ala Trp Leu Ser Leu
 225 230 235 240
 Phe Val Asn Trp Lys Val Ser Met Phe Val Glu Val His Lys Ala Ile
 245 250 255
 Lys Lys Arg Arg Arg Arg Arg Lys Glu Ser Phe Glu Ser Ser Pro His
 20 260 265 270
 Ser Arg Lys Ala Leu Gln Val Lys Gly Ser Thr Ala Ser Lys Asp Val
 275 280 285
 Asn Ile Phe Ser Phe Leu Ser Lys Lys Glu Glu Thr Tyr Asn Asp Leu
 290 295 300
 25 Ile Lys Gln Ile Gly Lys Lys Ala Met Lys Thr Ser Gly Gly Gly Glu
 305 310 315 320
 Thr Gly Pro Gly Pro Gly Leu Gly Pro Gln Gly Gly Gly Leu Pro Ala
 325 330 335
 Leu Pro Pro Ser Leu Val Pro Leu Val Val Tyr Ser Lys Asn Arg Val
 30 340 345 350
 Pro Thr Leu Glu Glu Val Ser Gln Thr Leu Arg Ser Lys Gly His Val
 355 360 365
 Ser Arg Ser Pro Asp Glu Glu Ala Val Ala Arg Ala Pro Glu Asp Ser
 370 375 380
 35 Ser Pro Ala Pro Glu Val Phe Met Asn Gln Leu Asp Arg Ile Ser Glu

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385 390 395 400
 Glu Cys Glu Pro Trp Asp Ala Gln Asp Tyr His Pro Leu Ile Phe Gln
 405 410 415
 Asp Ala Ser Ile Thr Phe Val Asn Thr Glu Ala Gly Leu Ser Asp Glu
 5 420 425 430
 Glu Thr Ser Lys Ser Ser Leu Glu Asp Asn Leu Ala Gly Glu Glu Ser
 435 440 445
 Pro Gln Gln Gly Ala Glu Ala Lys Ala Pro Leu Asn Met Gly Glu Phe
 450 455 460
 10 Pro Ser Ser Ser Glu Ser Thr Phe Thr Ser Thr Glu Ser Glu Leu Ser
 465 470 475 480
 Val Pro Tyr Glu Gln Leu Met Asn Glu Tyr Asn Lys Ala Asn Ser Pro
 485 490 495
 Lys Gly Thr
 15

 <210> 69
 <211> 106
 <212> PRT
 20 <213> Homo sapiens

 <400> 69
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 25 Ala Pro Phe Ala Gln Arg Ile Asp Pro Thr Arg Glu Lys Leu Thr Pro
 20 25 30
 Glu Gln Leu His Ser Met Arg Gln Ala Glu Leu Ala Gln Trp Gln Lys
 35 40 45
 Val Leu Pro Arg Arg Arg Thr Arg Asn Ile Val Thr Gly Leu Gly Ile
 30 50 55 60
 Gly Ala Leu Val Leu Ala Ile Tyr Gly Tyr Thr Phe Tyr Ser Ile Ser
 65 70 75 80
 Gln Glu Arg Phe Leu Asp Glu Leu Glu Asp Glu Ala Lys Ala Ala Arg
 85 90 95
 35 Ala Arg Ala Leu Ala Arg Ala Ser Gly Ser

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100

105

<210> 70

<211> 152

5 <212> PRT

<213> Homo sapiens

<400> 70

10 Met Asp Tyr Val Cys Cys Ala Tyr Asn Asn Ile Thr Gly Arg Gln Asp
 1 5 10 15
 Glu Thr His Phe Thr Val Ile Ile Thr Ser Val Gly Leu Glu Lys Leu
 20 25 30
 Ala Gln Lys Gly Lys Ser Leu Ser Pro Leu Ala Ser Ile Thr Gly Ile
 35 40 45
 15 Ser Leu Phe Leu Ile Ile Ser Met Cys Leu Leu Phe Leu Trp Lys Lys
 50 55 60
 Tyr Gln Pro Tyr Lys Val Ile Lys Gln Lys Leu Glu Gly Arg Pro Glu
 65 70 75 80
 Thr Glu Tyr Arg Lys Ala Gln Thr Phe Ser Gly His Glu Asp Ala Leu
 20 85 90 95
 Asp Asp Phe Gly Ile Tyr Glu Phe Val Ala Phe Pro Asp Val Ser Gly
 100 105 110
 Val Ser Arg Ile Pro Ser Arg Ser Val Pro Ala Ser Asp Cys Val Ser
 115 120 125
 25 Gly Gln Asp Leu His Ser Thr Val Tyr Glu Val Ile Gln His Ile Pro
 130 135 140
 Ala Gln Gln Gln Asp His Pro Glu
 145 150

30 <210> 71

<211> 921

<212> DNA

<213> Homo sapiens

35 <400> 71

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	atgtctatga ttttatctgc ctcagtcatt cgtgtcagag atggactgcc actttctgct	60
	tctactgatt atgaacaaag cacaggaatg caggagtga gaaagtattt taaaatgctt	120
	tcgaggaaac ttgtcact tcctgataga tgtacactga aaactggaca ttataacatt	180
	aattttatta gctctctggg agtgagctac atgatgttgt gcactgaaaa ttacccaaat	240
5	gttctcgcct tctctttcct ggatgagctt cagaaggagt tcattactac ttataacatg	300
	atgaagacaa atactgctgt cagaccatac tgtttcattg aatttgataa cttcattcag	360
	aggaccaagc agcgatataa taatcccagg tctctttcaa caaagataaa tctttctgac	420
	atgcagacgg aaatcaagct gaggcctcct tatcaaattt ccatgtgcga actggggtca	480
	gccaatggag tcacatcagc attttctgtt gactgtaaag gtgctggtaa gatttcttct	540
10	gtccaccagc gactggaacc agcaactctg tcagggattg taggatttat ccttagtctt	600
	ttatgtggag ctctgaattt aattcgaggc ttctcatgcta tagaaagtct cctgcagagt	660
	gatggtgatg attttaatta catcattgca ttttctctg gaacagcagc ctgcctttac	720
	cagtgttatt tacttgtcta ctacaccggc tggcggaatg tcaaatcttt ttgactttt	780
	ggcttaatct gtctatgcaa catgtatctc tatgaactgc gcaacctctg gcagcttttc	840
15	tttcatgtga ctgtgggagc atttgttaca ctacagatct ggctaaggca agcccagggc	900
	aaggetcccg attatgatgt c	921
	<210> 72	
	<211> 549	
20	<212> DNA	
	<213> Homo sapiens	
	<400> 72	
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25	ctaagcgggc ctggaggagg cagcaggggt cgaagtgacc ggggcagtgg ccaggagagac	120
	tcgctctacc cagtcggtta cttggacaag caagtgcctg ataccagcgt gcaagagaca	180
	gaccggatcc tgggtggagaa gcgctgctgg gacatgcctt tgggtccctt caaacagatt	240
	cccatgaatc tcttcatcat gtacatggca ggcaatacta tctccatctt ccctactatg	300
	atggtgtgta tgatggcctg gcgaccatt caggcaactta tggccatttc agccactttc	360
30	aagatgttag aaagttcaag ccagaagttt cttcaggggt tgggtctatct cattgggaac	420
	ctgatgggtt tggcattggc tgtttacaag tgccagtcca tgggactgtt acctacacat	480
	gcacgggatt gggttagcctt cattgagccc cctgagagaa tggagttag tgggtggagga	540
	ctgcttttg	549
35	<210> 73	

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<211> 981

<212> DNA

<213> Homo sapiens

5 <400> 73

	atgcgcgccc tccccggcct gctggaggcc agggcgcgta cggcccggct gctcctcctc	60
	cagtgccttc tcgctgccgc gcgcccagc tcggcgagc gcagtgcccc agattegcct	120
	tttacaagtc cacctctcag agaagaaata atggcaaata acttttcctt ggagagtcac	180
	aacatatcac tgactgaaca ttctagtatg ccagtagaaa aaaatatcac tttagaaagg	240
10	ccttctaata taaatctcac atgccagttc acaacatctg gggatttgaa tgcagtaaat	300
	gtgacttggg aaaaagatgg tgaacaactt gagaataatt atcttgtcag tgcaacagga	360
	agcaccttgt ataccaata caggttcacc atcattaata gcaaacaat gggaggttat	420
	tcttgtttct ttcgagagga aaaggaacaa aggggaacat ttaatttcaa agtccctgaa	480
	cttcattgga aaaacaagcc attgatctct tacgtagggg attctactgt cttgacatgt	540
15	aaatgtcaaa attgttttcc tttaaattgg acctggtaca gtagtaatgg gagtgtaaag	600
	gttccctgttg gtgttcaaata gaataaatat gtgatcaatg gaacatatgc taacgaaaca	660
	aagctgaaga taacacaact tttggaggaa gatggggaat cttactggtg ccgtgcacta	720
	ttccaattag gcgagagtga agaacacatt gagcttgtgg tgctgagcta tttggtgccc	780
	ctcaaaccat ttcttgtaat agtggtctgag gtgattcttt tagtggccac cattctgctt	840
20	tgtgaaaagt acacacaaaa gaaaaagaag cactcagatg aggggaaaga atttgagcag	900
	attgaacagc tgaaatcaga tgatagcaat ggtatagaaa ataatgtccc caggcataga	960
	aaaaatgagt ctctgggcca g	981

<210> 74

25 <211> 669

<212> DNA

<213> Homo sapiens

<400> 74

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	gccccgaggc aaaagcaagg aagcactggg gaggaattcc atttccagac tggagggaga	120
	gattcctgca ctatgcgtcc cagcagcttg gggcaagggtg ctggagaagt ctggcttcgc	180
	gtgactgccc gcaacacaga ccagacctac tgggtgtgagt acagggggca gccagcatg	240
	tgccaggctt tcgctgctga ccccaaactc tactggaatc aagccctgca ggagctgagg	300
35	cgccttcacc atgcgtgcca gggggccccg gtgcttaggc catccgtgtg caggagggt	360

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	ggaccccagg cccatatgca gcaggtgact tccagcctca agggcagccc agagcccaac	420
	cagcagcctg aggctgggac gccatctctg aggcccaagg ccacagtga actcacagaa	480
	gcaacacagc tgggaaagga ctcgatggaa gagctgggaa aagccaaacc caccacccga	540
	cccacagcca aacctaccca gcctggaccc agggccggag ggaatgagga agcaaagaag	600
5	aaggcctggg aacattgttg gaaacccttc caggccctgt gcgcctttct catcagcttc	660
	ttccgaggg	669
	<210> 75	
	<211> 144	
10	<212> DNA	
	<213> Homo sapiens	
	<400> 75	
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15	gccaatctgg gcggcgctgc cagcaagaga ttaaatgatgc agtacgccac ggggcgctg	120
	ctcaagttec agatttgtgt ttcc	144
	<210> 76	
	<211> 1113	
20	<212> DNA	
	<213> Homo sapiens	
	<400> 76	
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25	aacacgctct cggcaaaatg ggcggacaat ttcattggcg agggctgtgg agggagcaag	120
	gagcacagct tccagcatec ctccctccag gcagtgggca tgttcctggg agaattctcc	180
	tgcttggtg cttctacct cctccgatgc agagctgcag ggcaatcaga ctccagcgta	240
	gacccccage agcccttcaa cctcttctt ttctgcccc cagcgtcttg tgacatgaca	300
	gggaccagcc tcatgtatgt ggctctgaac atgaccagt cctccagctt ccagatgctg	360
30	cggggtgcag tgatcatatt cactggcctg ttctcggtgg ccttcctggg ccggaggctg	420
	gtgctgagcc agtggctggg catcctagcc accatcgcg ggctggtggt cgtgggcctg	480
	gctgacctcc tgagcaagca cgacagtac cacaagctca gcgaagtgat cacaggggac	540
	ctgttgatca tcatggccca gatcatcggt gccatccaga tggtgctaga ggagaagttc	600
	gtctacaaac acaatgtgca cccactgctg gcagttggca ctgagggcct ctttggtctt	660
35	gtgatcctct cctgctgct ggtgcccatt tactacatcc ccgccggctc ctccagcgga	720

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	aaccctcgtg ggacàctgga ggatgcattg gacgccttct gccaggtggg ccagcagccg	780
	ctcattgccg tggcactgct gggcaacatc agcagcattg ccttcttcaa cttegcaggc	840
	atcagcgtca ccaaggaact gagegccacc acccgcatgg tgttgacag cttgcgcacc	900
	gttgtcatct gggcactgag cctggcactg ggctgggagg ccttccatgc actgcagatc	960
5	cttggttcc tcatactcct tataggcact gccctctaca atgggctaca ccgtccgctg	1020
	ctgggccgcc tgtccagggg ccggcccctg gcagaggaga gcgagcagga gagactgctg	1080
	ggtggcaccc gcactcccat caatgatgcc agc	1113
	<210> 77	
10	<211> 270	
	<212> DNA	
	<213> Homo sapiens	
	<400> 77	
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	taccagtgcc ctgagcacag tcaactgaca actctgggag tggatgggaa ggagtccca	120
	gaggtccact tgggccagtg gtactttatc gcaggggcag ctcccaccaa ggaggagttg	180
	gcaacttttg accctgtgga caacattgtc ttcaatatgg ctgctggctc tgccccgatg	240
	cagctccacc ttcgtgctac catccgcatg	270
20	<210> 78	
	<211> 1497	
	<212> DNA	
	<213> Homo sapiens	
25	<400> 78	
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	gcgatcttcg aagtgtgga ggagccacac tggaggagg ccaagaaaa ctactacaca	120
	cagaagctgc atctgtcaa ggagtcccg tgcctgggtc aggagggcct ggacaagatc	180
30	ctagagggtg tatctgatgc tgcaggacag ggtgtggcca tcacaggga ccagaccttc	240
	aacaactgga actggcccaa tgcaatgatt ttgcagcga ccgtcattac caccattgga	300
	tatggcaatg tggtcccaa gacccccgcc ggtgcctct tctgtgttt ctatggtctc	360
	ttcgggtgct cgctctgcct gacgtggatc agtgccctgg gcaagttctt cgggggacgt	420
	gccaaagagac tagggcagtt ccttaccag agaggtgtga gtctgcgga ggccagatc	480
35	acgtgcacag tcattctcat cgtgtggggc gtcctagtc accctggtgat cccaccttc	540

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 gccctgtacc gctacttcgt ggagctctgg atctacttgg ggctggcctg gctgtccctt 720
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 gggagcacag cctccaagga cgtcaacatc ttcagctttc tttccaagaa ggaagagacc 900
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 gacaacttgg caggggagga gagccccag cagggggctg aagccaaggc gcccctgaac 1380
 15 atgggcgagt tcccctctc ctccgagtcc accttcacca gactgagtc tgagctctct 1440
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<211> 318

20 <212> DNA

<213> Homo sapiens

<400> 79

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 25 cagcgtatcg acccgactcg ggagaagctg acaccgagc aactgcattc catgeggag 120
 gcggagcttg cccagtggca gaaggtccta ccacggcggc gaaccgggaa catcgtgacc 180
 ggcctaggca tcggggccct ggtgttggt atttatggtt acaccttcta ctcgatttcc 240
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 gcaagggcgt cagggtcc 318

30

<210> 80

<211> 456

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<213> Homo sapiens

35

80/177

<400> 80

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 cctttagcaa gtataactgg aatatcacta tttttgatta tatccatgtg tcttctcttc 180
 5 ctatggaaaa aatatcaacc ctacaaagtt ataaaacaga aactagaagg caggccagaa 240
 acagaatata ggaaagctca aacattttca ggccatgaag atgctctgga tgacttcgga 300
 atatatgaat ttgttgcttt tccagatgtt tctggtgttt ccaggatccc aagcaggtct 360
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10

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<211> 1436

<212> DNA

<213> Homo sapiens

15

<220>

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<222> (66)...(989)

<400> 81

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 Met Ser Met Ile Leu Ser Ala Ser Val Ile Arg Val Arg Asp
 1 5 10
 gga ctg cca ctt tct gct tct act gat tat gaa caa agc aca gga atg 155
 25 Gly Leu Pro Leu Ser Ala Ser Thr Asp Tyr Glu Gln Ser Thr Gly Met
 15 20 25 30
 cag gag tgc aga aag tat ttt aaa atg ctt tcg agg aaa ctt gct caa 203
 Gln Glu Cys Arg Lys Tyr Phe Lys Met Leu Ser Arg Lys Leu Ala Gln
 35 40 45
 30 ctt cct gat aga tgt aca ctg aaa act gga cat tat aac att aat ttt 251
 Leu Pro Asp Arg Cys Thr Leu Lys Thr Gly His Tyr Asn Ile Asn Phe
 50 55 60
 att agc tct ctg gga gtg agc tac atg atg ttg tgc act gaa aat tac 299
 Ile Ser Ser Leu Gly Val Ser Tyr Met Met Leu Cys Thr Glu Asn Tyr
 35 65 70 75

81/177

	cca aat gtt ctc gcc ttc tct ttc ctg gat gag ctt cag aag gag ttc	347
	Pro Asn Val Leu Ala Phe Ser Phe Leu Asp Glu Leu Gln Lys Glu Phe	
	80 85 90	
	att act act tat aac atg atg aag aca aat act gct gtc aga cca tac	395
5	Ile Thr Thr Tyr Asn Met Met Lys Thr Asn Thr Ala Val Arg Pro Tyr	
	95 100 105 110	
	tgt ttc att gaa ttt gat aac ttc att cag agg acc aag cag cga tat	443
	Cys Phe Ile Glu Phe Asp Asn Phe Ile Gln Arg Thr Lys Gln Arg Tyr	
	115 120 125	
10	aat aat ccc agg tct ctt tca aca aag ata aat ctt tct gac atg cag	491
	Asn Asn Pro Arg Ser Leu Ser Thr Lys Ile Asn Leu Ser Asp Met Gln	
	130 135 140	
	acg gaa atc aag ctg agg cct cct tat caa att tcc atg tgc gaa ctg	539
	Thr Glu Ile Lys Leu Arg Pro Pro Tyr Gln Ile Ser Met Cys Glu Leu	
15	145 150 155	
	ggg tca gcc aat gga gtc aca tca gca ttt tct gtt gac tgt aaa ggt	587
	Gly Ser Ala Asn Gly Val Thr Ser Ala Phe Ser Val Asp Cys Lys Gly	
	160 165 170	
	gct ggt aag att tct tct gct cac cag cga ctg gaa cca gca act ctg	635
20	Ala Gly Lys Ile Ser Ser Ala His Gln Arg Leu Glu Pro Ala Thr Leu	
	175 180 185 190	
	tca ggg att gta gga ttt atc ctt agt ctt tta tgt gga gct ctg aat	683
	Ser Gly Ile Val Gly Phe Ile Leu Ser Leu Leu Cys Gly Ala Leu Asn	
	195 200 205	
25	tta att cga ggc ttt cat gct ata gaa agt ctc ctg cag agt gat ggt	731
	Leu Ile Arg Gly Phe His Ala Ile Glu Ser Leu Leu Gln Ser Asp Gly	
	210 215 220	
	gat gat ttt aat tac atc att gca ttt ttc ctt gga aca gca gcc tgc	779
	Asp Asp Phe Asn Tyr Ile Ile Ala Phe Phe Leu Gly Thr Ala Ala Cys	
30	225 230 235	
	ctt tac cag tgt tat tta ctt gtc tac tac acc ggc tgg cgg aat gtc	827
	Leu Tyr Gln Cys Tyr Leu Leu Val Tyr Tyr Thr Gly Trp Arg Asn Val	
	240 245 250	
	aaa tct ttt ttg act ttt ggc tta atc tgt cta tgc aac atg tat ctc	875
35	Lys Ser Phe Leu Thr Phe Gly Leu Ile Cys Leu Cys Asn Met Tyr Leu	

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	255	260	265	270	
	tat gaa ctg cgc aac ctc tgg cag ctt ttc ttt cat gtg act gtg gga				923
	Tyr Glu Leu Arg Asn Leu Trp Gln Leu Phe Phe His Val Thr Val Gly				
		275	280	285	
5	gca ttt gtt aca cta cag atc tgg cta agg caa gcc cag ggc aag gct				971
	Ala Phe Val Thr Leu Gln Ile Trp Leu Arg Gln Ala Gln Gly Lys Ala				
		290	295	300	
	ccc gat tat gat gtc tgacaccatc cttcagatct attgccttgg cttc				1020
	Pro Asp Tyr Asp Val				
10		305			
	agggggataa ggagggaaca tatcataact gcactgtgat gaagaagctg ttccccacag				1080
	aggagaagct ctgctttctt tctctccaac tttccttttt taaaatcagc atgatgtgcc				1140
	tgtgagcatg gaagagtcct ctcagaagaa tgttggccat gagactatca ttcagaggag				1200
	gaggggattt ctctettcaa ggccataaca gtggaagaac agtcatatgc cattggaagt				1260
15	cttgccagc agtcctgaat ccttcctgaa gagttcagaa aatagatgtg gtattgotct				1320
	gaggaccagg caggaggaac tctacaacct gagtttgccct ttgtgaggca ttagtataga				1380
	ccaaataaaa agctgcagaa attggaaagt ttatgtttta aataaatgac tgtgat				1436
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	cgaggctata ggacgcagct gttgcc atg acg gcc cag ggg ggc ctg gtg				110
30		Met Thr Ala Gln Gly Gly Leu Val			
		1	5		
	gct aac cga ggc cgg cgc ttc aag tgg gcc att gag cta agc ggg cct				158
	Ala Asn Arg Gly Arg Arg Phe Lys Trp Ala Ile Glu Leu Ser Gly Pro				
		10	15	20	
35	gga gga ggc agc agg ggt cga agt gac cgg ggc agt ggc cag gga gac				206

	Gly Gly Gly Ser Arg Gly Arg Ser Asp Arg Gly Ser Gly Gln Gly Asp	
	25 30 35 40	
	tcg ctc tac cca gtc ggt tac ttg gac aag caa gtg cct gat acc agc	254
5	Ser Leu Tyr Pro Val Gly Tyr Leu Asp Lys Gln Val Pro Asp Thr Ser	
	45 50 55	
	gtg caa gag aca gac cgg atc ctg gtg gag aag cgc tgc tgg gac atc	302
	Val Gln Glu Thr Asp Arg Ile Leu Val Glu Lys Arg Cys Trp Asp Ile	
	60 65 70	
10	gcc ttg ggt ccc ctc aaa cag att ccc atg aat ctc ttc atc atg tac	350
	Ala Leu Gly Pro Leu Lys Gln Ile Pro Met Asn Leu Phe Ile Met Tyr	
	75 80 85	
	atg gca ggc aat act atc tcc atc ttc cct act atg atg gtg tgt atg	398
	Met Ala Gly Asn Thr Ile Ser Ile Phe Pro Thr Met Met Val Cys Met	
	90 95 100	
15	atg gcc tgg cga ccc att cag gca ctt atg gcc att tca gcc act ttc	446
	Met Ala Trp Arg Pro Ile Gln Ala Leu Met Ala Ile Ser Ala Thr Phe	
	105 110 115 120	
	aag atg tta gaa agt tca agc cag aag ttt ctt cag ggt ttg gtc tat	494
	Lys Met Leu Glu Ser Ser Ser Gln Lys Phe Leu Gln Gly Leu Val Tyr	
20	125 130 135	
	ctc att ggg aac ctg atg ggt ttg gca ttg gct gtt tac aag tgc cag	542
	Leu Ile Gly Asn Leu Met Gly Leu Ala Leu Ala Val Tyr Lys Cys Gln	
	140 145 150	
25	tcc atg gga ctg tta cct aca cat gca tcg gat tgg tta gcc ttc att	590
	Ser Met Gly Leu Leu Pro Thr His Ala Ser Asp Trp Leu Ala Phe Ile	
	155 160 165	
	gag ccc cct gag aga atg gag ttc agt ggt gga gga ctg ctt ttg tgaac	640
	Glu Pro Pro Glu Arg Met Glu Phe Ser Gly Gly Gly Leu Leu Leu	
	170 175 180	
30	atgagaaagc agcgccctggt ccctatgtat ttgggtctta tttacatcct tctttaagcc	700
	cagtggctcc tcagcatact cttaaactaa tcacttatgt taaaaagaac caaaagactc	760
	ttttctccat ggtggggtga caggtcctag aaggacaatg tgcatattac gacaaacaca	820
	aagaaactat accataaccc aaggetgaaa ataatgtaga aaactttatt tttgtttcca	880
	gtacagagca aaacaacaac aaaaaaacat aactatgtaa acaagagaat aactgctgct	940
35	aatcaagaa ctgttgacgc atctcctttc aataaattaa atggttgaga acaatgc	997

84/177

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 5 <213> Homo sapiens
 <220>
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 accctctggc gcc atg cgc gcc ctc ccc ggc ctg ctg gag gcc agg gcg 169
 Met Arg Ala Leu Pro Gly Leu Leu Glu Ala Arg Ala
 15 1 5 10
 cgt acg ccc egg ctg ctc ctc ctc cag tgc ctt ctc gct gcc gcg cgc 217
 Arg Thr Pro Arg Leu Leu Leu Leu Gln Cys Leu Leu Ala Ala Ala Arg
 15 20 25
 cca agc tcg gcg gac ggc agt gcc cca gat tcg cct ttt aca agt cca 265
 20 Pro Ser Ser Ala Asp Gly Ser Ala Pro Asp Ser Pro Phe Thr Ser Pro
 30 35 40
 cct ctc aga gaa gaa ata atg gca aat aac ttt tcc ttg gag agt cat 313
 Pro Leu Arg Glu Glu Ile Met Ala Asn Asn Phe Ser Leu Glu Ser His
 45 50 55 60
 25 aac ata tca ctg act gaa cat tct agt atg cca gta gaa aaa aat atc 361
 Asn Ile Ser Leu Thr Glu His Ser Ser Met Pro Val Glu Lys Asn Ile
 65 70 75
 act tta gaa agg cct tct aat gta aat ctc aca tgc cag ttc aca aca 409
 Thr Leu Glu Arg Pro Ser Asn Val Asn Leu Thr Cys Gln Phe Thr Thr
 30 80 85 90
 tct ggg gat ttg aat gca gta aat gtg act tgg aaa aaa gat ggt gaa 457
 Ser Gly Asp Leu Asn Ala Val Asn Val Thr Trp Lys Lys Asp Gly Glu
 95 100 105
 caa ctt gag aat aat tat ctt gtc agt gca aca gga agc acc ttg tat 505
 35 Gln Leu Glu Asn Asn Tyr Leu Val Ser Ala Thr Gly Ser Thr Leu Tyr

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	110	115	120	
	acc caa tac agg ttc acc atc att aat agc aaa caa atg gga agt tat			553
	Thr Gln Tyr Arg Phe Thr Ile Ile Asn Ser Lys Gln Met Gly Ser Tyr			
	125	130	135	140
5	tct tgt ttc ttt cga gag gaa aag gaa caa agg gga aca ttt aat ttc			601
	Ser Cys Phe Phe Arg Glu Glu Lys Glu Gln Arg Gly Thr Phe Asn Phe			
	145	150	155	
	aaa gtc cct gaa ctt cat ggg aaa aac aag cca ttg atc tct tac gta			649
	Lys Val Pro Glu Leu His Gly Lys Asn Lys Pro Leu Ile Ser Tyr Val			
10	160	165	170	
	ggg gat tct act gtc ttg aca tgt aaa tgt caa aat tgt ttt cct tta			697
	Gly Asp Ser Thr Val Leu Thr Cys Lys Cys Gln Asn Cys Phe Pro Leu			
	175	180	185	
	aat tgg acc tgg tac agt agt aat ggg agt gta aag gtt cct gtt ggt			745
15	Asn Trp Thr Trp Tyr Ser Ser Asn Gly Ser Val Lys Val Pro Val Gly			
	190	195	200	
	gtt caa atg aat aaa tat gtg atc aat gga aca tat gct aac gaa aca			793
	Val Gln Met Asn Lys Tyr Val Ile Asn Gly Thr Tyr Ala Asn Glu Thr			
	205	210	215	220
20	aag ctg aag ata aca caa ctt ttg gag gaa gat ggg gaa tct tac tgg			841
	Lys Leu Lys Ile Thr Gln Leu Leu Glu Glu Asp Gly Glu Ser Tyr Trp			
	225	230	235	
	tgc cgt gca cta ttc caa tta ggc gag agt gaa gaa cac att gag ctt			889
	Cys Arg Ala Leu Phe Gln Leu Gly Glu Ser Glu Glu His Ile Glu Leu			
25	240	245	250	
	gtg gtg ctg agc tat ttg gtg ccc ctc aaa cca ttt ctt gta ata gtg			937
	Val Val Leu Ser Tyr Leu Val Pro Leu Lys Pro Phe Leu Val Ile Val			
	255	260	265	
	gct gag gtg att ctt tta gtg gcc acc att ctg ctt tgt gaa aag tac			985
30	Ala Glu Val Ile Leu Leu Val Ala Thr Ile Leu Leu Cys Glu Lys Tyr			
	270	275	280	
	aca caa aag aaa aag aag cac tca gat gag ggg aaa gaa ttt gag cag			1033
	Thr Gln Lys Lys Lys Lys His Ser Asp Glu Gly Lys Glu Phe Glu Gln			
	285	290	295	300
35	att gaa cag ctg aaa tca gat gat agc aat ggt ata gaa aat aat gtc			1081

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Ile Glu Gln Leu Lys Ser Asp Asp Ser Asn Gly Ile Glu Asn Asn Val
305 310 315
ccc agg cat aga aaa aat gag tct ctg ggc cag tgaatacaaaa acatca 1130
Pro Arg His Arg Lys Asn Glu Ser Leu Gly Gln
5 320 325
tgtcgcagaat cattggaaga tatacagagt tegtattttca gctttatttta tcttctctgt 1190
taagagcctc tgagttttta gttttaaaag gatgaaaagc ttatgcaaca tgctcagcag 1250
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Met Lys Phe Val Pro Cys Leu Leu Leu Val Thr Leu Ser Cys Leu
30 1 5 10 15
ggg act ttg ggt cag gcc ccg agg caa aag caa gga agc act ggg gag 154
Gly Thr Leu Gly Gln Ala Pro Arg Gln Lys Gln Gly Ser Thr Gly Glu
20 25 30
gaa ttc cat ttc cag act gga ggg aga gat tcc tgc act atg cgt ccc 202
35 Glu Phe His Phe Gln Thr Gly Gly Arg Asp Ser Cys Thr Met Arg Pro

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	35	40	45	
	agc agc ttg ggg caa ggt gct gga gaa gtc tgg ctt cgc gtc gac tgc			250
	Ser Ser Leu Gly Gln Gly Ala Gly Glu Val Trp Leu Arg Val Asp Cys			
	50	55	60	
5	cgc aac aca gac cag acc tac tgg tgt gag tac agg ggg cag ccc agc			298
	Arg Asn Thr Asp Gln Thr Tyr Trp Cys Glu Tyr Arg Gly Gln Pro Ser			
	65	70	75	
	atg tgc cag gct ttc gct gct gac ccc aaa tct tac tgg aat caa gcc			346
	Met Cys Gln Ala Phe Ala Ala Asp Pro Lys Ser Tyr Trp Asn Gln Ala			
10	80	85	90	95
	ctg cag gag ctg agg cgc ctt cac cat gcg tgc cag ggg gcc ccg gtg			394
	Leu Gln Glu Leu Arg Arg Leu His His Ala Cys Gln Gly Ala Pro Val			
	100	105	110	
	ctt agg cca tcc gtg tgc agg gag gct gga ccc cag gcc cat atg cag			442
15	Leu Arg Pro Ser Val Cys Arg Glu Ala Gly Pro Gln Ala His Met Gln			
	115	120	125	
	cag gtg act tcc agc ctc aag ggc agc cca gag ccc aac cag cag cct			490
	Gln Val Thr Ser Ser Leu Lys Gly Ser Pro Glu Pro Asn Gln Gln Pro			
	130	135	140	
20	gag gct ggg acg cca tct ctg agg ccc aag gcc aca gtg aaa ctc aca			538
	Glu Ala Gly Thr Pro Ser Leu Arg Pro Lys Ala Thr Val Lys Leu Thr			
	145	150	155	
	gaa gca aca cag ctg gga aag gac tcg atg gaa gag ctg gga aaa gcc			586
	Glu Ala Thr Gln Leu Gly Lys Asp Ser Met Glu Glu Leu Gly Lys Ala			
25	160	165	170	175
	aaa ccc acc acc cga ccc aca gcc aaa cct acc cag cct gga ccc agg			634
	Lys Pro Thr Thr Arg Pro Thr Ala Lys Pro Thr Gln Pro Gly Pro Arg			
	180	185	190	
	ccc gga ggg aat gag gaa gca aag aag aag gcc tgg gaa cat tgt tgg			682
30	Pro Gly Gly Asn Glu Glu Ala Lys Lys Lys Ala Trp Glu His Cys Trp			
	195	200	205	
	aaa ccc ttc cag gcc ctg tgc gcc ttt ctc atc agc ttc ttc cga ggg			730
	Lys Pro Phe Gln Ala Leu Cys Ala Phe Leu Ile Ser Phe Phe Arg Gly			
	210	215	220	
35	tgacaggtga aagacccta cagatctgac ctctccctga cagacaacca tctcttttta			790

	tattatgccg ctttcaatcc aacgttctca cactggaaga agagagtttc taatcagatg	850
	caacggccca aattcttgat ctgcagcttc tctgaagttt ggaaaagaaa ccttcctttc	910
	tggagtttgc agagttcagc aatatgatag ggaacaggtg ctgatgggcc caagagtgac	970
	aagcatacac aactacttat tatctgtaga agttttgett tgttgatctg agccttctat	1030
5	gaaagtttaa atatgtaacg cattcatgaa tttccagtgt tcagtaaata gcagctatgt	1090
	gtgtgcaaaa taaaagaatg atttcag	1117

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<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (43)...(189)

15

<400> 85

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Met Arg Leu Leu

1

ctg ctt ctc cta gtg gcg gcg tct gcg atg gtc cgg agc gag gcc tcg 102
Leu Leu Leu Leu Val Ala Ala Ser Ala Met Val Arg Ser Glu Ala Ser
5 10 15 20

gcc aat ctg ggc ggc gtg ccc agc aag aga tta aag atg cag tac gcc 150
Ala Asn Leu Gly Gly Val Pro Ser Lys Arg Leu Lys Met Gln Tyr Ala

	25	30	35	
acg ggg ccg ctg ctc aag ttc cag att tgt gtt tcc tgag				190
Thr Gly Pro Leu Leu Lys Phe Gln Ile Cys Val Ser				

40

45

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gcattgaagg	agagaattac	ctccctcaac	caatatatag	acacatagca	tctttcctgt	310
cagtcttcaa	actagtatta	ataggcttaa	taattgttg	caaggatcct	tttgctttct	370
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tgatggtttt	cttcttgagc	aacatgattg	agaaccagt	tatgtcaaca	ggtgcatttg	490
agataacttt	aaatgatgta	cctgtgtggt	ctaagctgga	atctggtcac	cttccatcca	550
tgcaacaact	tgttcaaatt	cttgacaatg	aaatgaagct	caatgtgcat	atggattcaa	610

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	tcccacacca	tcgatcatag	caccacctat	cagcactgaa	aactcttttg	cattaaggga	670
	tcattgcaag	agcagcgtga	ctgacattat	gaaggcctgt	actgaagaca	gcaagctggt	730
	agtacagacc	agatgctttc	ttggcaggct	cgttgtagct	cttggaanaac	ctcaatgcaa	790
	gatagtgttt	cagtgtgtgc	atatttttga	attctgcaca	ttcatggagt	gcaataatac	850
5	tgtatagctt	tccccacctc	ccacaaaatc	accaggttaa	tgtgtgtgtg	tggttttttt	910
	tttaaggtaa	acattactac	ttgtaacttt	ttttcttagt	catatttgaa	aaagtagaaa	970
	attgagttac	aatttgattt	tttttccaaa	gatgtctgtt	aaatctgttg	tgctttttata	1030
	tgaatatttg	ttttttatag	tttaaaattg	atcctttggg	aatccagttg	aagttcccaa	1090
	atactttata	agagttttatc	agacatctct	aatttgacca	tgtccagttt	atacagttta	1150
10	caaaatatag	cagatgcaag	attatggggg	aaatcctata	ttcagagtac	tctataaatt	1210
	tttgtgtatg	tgtgtatgtg	cgtgtgatta	ccagagaact	actaaaaaaaa	ccaactgctt	1270
	tttaaactct	attgtgtagt	taaagtgtca	tgcttgacc	aatctaata	attgattaat	1330
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	Trp Thr Lys	Tyr Gln	Leu Phe	Leu Ala	Gly Leu	Met Leu	Val Thr
	5		10		15		
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	Ser Ile Asn	Thr Leu	Ser Ala	Lys Trp	Ala Asp	Asn Phe	Met Ala
	20		25		30		
	ggc tgt gga	ggg agc	aag gag	cac agc	ttc cag	cat ccc	ttc ctc
	Gly Cys Gly	Gly Ser	Lys Glu	His Ser	Phe Gln	His Pro	Phe Leu
35	35		40		45		50

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	Ala Val Gly Met Phe Leu Gly Glu Phe Ser Cys Leu Ala Ala Phe Tyr	
	55 60 65	
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	Leu Leu Arg Cys Arg Ala Ala Gly Gln Ser Asp Ser Ser Val Asp Pro	
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	cag cag ccc ttc aac cct ctt ctt ttc ctg ccc cca gcg ctc tgt gac	344
	Gln Gln Pro Phe Asn Pro Leu Leu Phe Leu Pro Pro Ala Leu Cys Asp	
	85 90 95	
10	atg aca ggg acc agc ctc atg tat gtg gct ctg aac atg acc agt gcc	392
	Met Thr Gly Thr Ser Leu Met Tyr Val Ala Leu Asn Met Thr Ser Ala	
	100 105 110	
	tcc agc ttc cag atg ctg cgg ggt gca gtg atc ata ttc act ggc ctg	440
	Ser Ser Phe Gln Met Leu Arg Gly Ala Val Ile Ile Phe Thr Gly Leu	
15	115 120 125 130	
	ttc tcg gtg gcc ttc ctg ggc cgg agg ctg gtg ctg agc cag tgg ctg	488
	Phe Ser Val Ala Phe Leu Gly Arg Arg Leu Val Leu Ser Gln Trp Leu	
	135 140 145	
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	150 155 160	
	ctc ctg agc aag cac gac agt cag cac aag ctc agc gaa gtg atc aca	584
	Leu Leu Ser Lys His Asp Ser Gln His Lys Leu Ser Glu Val Ile Thr	
	165 170 175	
25	ggg gac ctg ttg atc atc atg gcc cag atc atc gtt gcc atc cag atg	632
	Gly Asp Leu Leu Ile Ile Met Ala Gln Ile Ile Val Ala Ile Gln Met	
	180 185 190	
	gtg cta gag gag aag ttc gtc tac aaa cac aat gtg cac cca ctg cgg	680
	Val Leu Glu Glu Lys Phe Val Tyr Lys His Asn Val His Pro Leu Arg	
30	195 200 205 210	
	gca gtt ggc act gag ggc ctc ttt ggc ttt gtg atc ctc tcc ctg ctg	728
	Ala Val Gly Thr Glu Gly Leu Phe Gly Phe Val Ile Leu Ser Leu Leu	
	215 220 225	
	ctg gtg ccc atg tac tac atc ccc gcc ggc tcc ttc agc gga aac cct	776
35	Leu Val Pro Met Tyr Tyr Ile Pro Ala Gly Ser Phe Ser Gly Asn Pro	

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	230	235	240	
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	Arg Gly Thr Leu Glu Asp Ala Leu Asp Ala Phe Cys Gln Val Gly Gln			
	245	250	255	
5	cag ccg ctc att gcc gtg gca ctg ctg ggc aac atc agc agc att gcc			872
	Gln Pro Leu Ile Ala Val Ala Leu Leu Gly Asn Ile Ser Ser Ile Ala			
	260	265	270	
	ttc ttc aac ttc gca ggc atc agc gtc acc aag gaa ctg agc gcc acc			920
	Phe Phe Asn Phe Ala Gly Ile Ser Val Thr Lys Glu Leu Ser Ala Thr			
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	acc cgc atg gtg ttg gac agc ttg cgc acc gtt gtc atc tgg gca ctg			968
	Thr Arg Met Val Leu Asp Ser Leu Arg Thr Val Val Ile Trp Ala Leu			
	295	300	305	
	agc ctg gca ctg ggc tgg gag gcc ttc cat gca ctg cag atc ctt ggc			1016
15	Ser Leu Ala Leu Gly Trp Glu Ala Phe His Ala Leu Gln Ile Leu Gly			
	310	315	320	
	ttc ctc ata ctc ctt ata ggc act gcc ctc tac aat ggg cta cac cgt			1064
	Phe Leu Ile Leu Leu Ile Gly Thr Ala Leu Tyr Asn Gly Leu His Arg			
	325	330	335	
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	Pro Leu Leu Gly Arg Leu Ser Arg Gly Arg Pro Leu Ala Glu Glu Ser			
	340	345	350	
	gag cag gag aga ctg ctg ggt ggc acc cgc act ccc atc aat gat gcc			1160
	Glu Gln Glu Arg Leu Leu Gly Gly Thr Arg Thr Pro Ile Asn Asp Ala			
25	355	360	365	370
	agc tgagggtccc tggaggcttc tactgccacc cgggtgctcc ttctccc			1210
	Ser			
	tgagactgag gccacacagg ctggtgggcc ccgaatgccc tatccccaag gcctcaccct			1270
30	gtccctccc tgcagaaccc ccagggcagc tgctgccaca gaagataaca acacccaagt			1330
	cctctttttc tcaactaccac ctgcaggggtg gtgttaccca gccccacaa gcctgagtgc			1390
	agtggcagac ctcagctctc tggaccctc ctacagcact agagctaaat catgaagttg			1450
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	Trp Ala Ala Leu Leu Tyr Phe Tyr Gly Ile Ile Leu Asn Ser Ile Tyr	
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15	cag tgc cct gag cac agt caa ctg aca act ctg ggc gtg gat ggg aag	150
	Gln Cys Pro Glu His Ser Gln Leu Thr Thr Leu Gly Val Asp Gly Lys	
	25 30 35	
	gag ttc cca gag gtc cac ttg ggc cag tgg tac ttt atc gca ggg gca	198
	Glu Phe Pro Glu Val His Leu Gly Gln Trp Tyr Phe Ile Ala Gly Ala	
20	40 45 50	
	gct ccc acc aag gag gag ttg gca act ttt gac cct gtg gac aac att	246
	Ala Pro Thr Lys Glu Glu Leu Ala Thr Phe Asp Pro Val Asp Asn Ile	
	55 60 65	
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	Val Phe Asn Met Ala Ala Gly Ser Ala Pro Met Gln Leu His Leu Arg	
	70 75 80 85	
	gct acc atc cgc atg tgagtggaaa gatgggctct gtgtgccccg g	340
	Ala Thr Ile Arg Met	
	90	
30	aaatggatct accacctgac tgaagggagc acagatctca gaactgaagg ccgccctgac	400
	atgaagactg agctcttttc cagctcatgc ccagggtggaa tcatgctgaa tgagacaggc	460
	cagggttacc agcgctttct cctctacaat cgtcaccac atcctccga aaagtgtgtg	520
	gaggaattca agtcctgac ttctgcctg gactccaaag ccttcttatt gactcctagg	580
	aatcaagagg cctgtgagct gtccaataac tgacctgtaa cttcatctaa gtccccagat	640
35	gggtacaatg ggagctgagt tgttgaggagg agaagctgga gacttcagc tccagctccc	700

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	tgggtgttcgc ccaccccggg ccgcgtgagt ggggccccac gcagctcccc gcactccgtg	180
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	cactgcgcac gcggagctcc aaattcaaac agctgttttc agaggctgga gggcgggcgg	300
	actggttagca gctgggggcta ggagaggctt tctctaggag gcggccgctc gggagcc	357
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	Met Val Asp Arg Gly Pro Leu Leu Thr Ser Ala Ile Ile Phe Tyr Leu	
	1 5 10 15	
	gcc atc ggg gcg gcg atc ttc gaa gtg ctg gag gag cca cac tgg aag	453
	Ala Ile Gly Ala Ala Ile Phe Glu Val Leu Glu Glu Pro His Trp Lys	
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	gag gcc aag aaa aac tac tac aca cag aag ctg cat ctg etc aag gag	501
	Glu Ala Lys Lys Asn Tyr Tyr Thr Gln Lys Leu His Leu Leu Lys Glu	
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	ttc ccg tgc ctg ggt cag gag ggc ctg gac aag atc cta gag gtg gta	549
30	Phe Pro Cys Leu Gly Gln Glu Gly Leu Asp Lys Ile Leu Glu Val Val	
	50 55 60	
	tct gat gct gca gga cag ggt gtg gcc atc aca ggg aac cag acc ttc	597
	Ser Asp Ala Ala Gly Gln Gly Val Ala Ile Thr Gly Asn Gln Thr Phe	
	65 70 75 80	
35	aac aac tgg aac tgg ccc aat gca atg att ttt gca gcg acc gtc att	645

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	Asn Asn Trp Asn Trp Pro Asn Ala Met Ile Phe Ala Ala Thr Val Ile	
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	acc acc att gga tat ggc aat gtg gct ccc aag acc ccc gcc ggt cgc	693
	Thr Thr Ile Gly Tyr Gly Asn Val Ala Pro Lys Thr Pro Ala Gly Arg	
5	100 105 110	
	ctc ttc tgt gtt ttc tat ggt ctc ttc ggg gtg ccg ctc tgc ctg acg	741
	Leu Phe Cys Val Phe Tyr Gly Leu Phe Gly Val Pro Leu Cys Leu Thr	
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	tgg atc agt gcc ctg ggc aag ttc ttc ggg gga cgt gcc aag aga cta	789
10	Trp Ile Ser Ala Leu Gly Lys Phe Phe Gly Gly Arg Ala Lys Arg Leu	
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	ggg cag ttc ctt acc aag aga ggt gtg agt ctg cgg aag gcg cag atc	837
	Gly Gln Phe Leu Thr Lys Arg Gly Val Ser Leu Arg Lys Ala Gln Ile	
	145 150 155 160	
15	acg tgc aca gtc atc ttc atc gtg tgg ggc gtc cta gtc cac ctg gtg	885
	Thr Cys Thr Val Ile Phe Ile Val Trp Gly Val Leu Val His Leu Val	
	165 170 175	
	atc cca ccc ttc gta ttc atg gtg act gag ggg tgg aac tac atc gag	933
	Ile Pro Pro Phe Val Phe Met Val Thr Glu Gly Trp Asn Tyr Ile Glu	
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	Gly Leu Tyr Tyr Ser Phe Ile Thr Ile Ser Thr Ile Gly Phe Gly Asp	
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25	Phe Val Ala Gly Val Asn Pro Ser Ala Asn Tyr His Ala Leu Tyr Arg	
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	Tyr Phe Val Glu Leu Trp Ile Tyr Leu Gly Leu Ala Trp Leu Ser Leu	
	225 230 235 240	
30	ttt gtc aac tgg aag gtg agc atg ttt gtg gaa gtc cac aaa gcc att	1125
	Phe Val Asn Trp Lys Val Ser Met Phe Val Glu Val His Lys Ala Ile	
	245 250 255	
	aag aag cgg cgg cgg cga cgg aag gag tcc ttt gag agc tcc cca cac	1173
	Lys Lys Arg Arg Arg Arg Arg Lys Glu Ser Phe Glu Ser Ser Pro His	
35	260 265 270	

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	tcc cgg aag gcc ctg cag gtg aag ggg agc aca gcc tcc aag gac gtc	1221
	Ser Arg Lys Ala Leu Gln Val Lys Gly Ser Thr Ala Ser Lys Asp Val	
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	Asn Ile Phe Ser Phe Leu Ser Lys Lys Glu Glu Thr Tyr Asn Asp Leu	
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	atc aag cag atc ggg aag aag gcc atg aag aca agc ggg ggt ggg gag	1317
	Ile Lys Gln Ile Gly Lys Lys Ala Met Lys Thr Ser Gly Gly Gly Glu	
	305 310 315 320	
10	acg ggc ccg ggc cca ggg ctg ggg cct caa ggc ggt ggg ctc cca gca	1365
	Thr Gly Pro Gly Pro Gly Leu Gly Pro Gln Gly Gly Gly Leu Pro Ala	
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	ctg ccc cct tcc ctg gtg ccc ctg gta gtc tac tcc aag aac cgg gtg	1413
	Leu Pro Pro Ser Leu Val Pro Leu Val Val Tyr Ser Lys Asn Arg Val	
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	ccc acc ttg gaa gag gtg tca cag aca ctg agg agc aaa ggc cac gta	1461
	Pro Thr Leu Glu Glu Val Ser Gln Thr Leu Arg Ser Lys Gly His Val	
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	tca agg tcc cca gat gag gag gct gtg gca cgg gcc cct gaa gac agc	1509
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	370 375 380	
	tcc cct gcc ccc gag gtg ttc atg aac cag ctg gac cgc atc agc gag	1557
	Ser Pro Ala Pro Glu Val Phe Met Asn Gln Leu Asp Arg Ile Ser Glu	
	385 390 395 400	
25	gaa tgc gag cca tgg gac gcc cag gac tac cac cca ctc atc ttc cag	1605
	Glu Cys Glu Pro Trp Asp Ala Gln Asp Tyr His Pro Leu Ile Phe Gln	
	405 410 415	
	gac gcc agc atc acc ttc gtg aac acg gag gct ggc ctc tca gac gag	1653
	Asp Ala Ser Ile Thr Phe Val Asn Thr Glu Ala Gly Leu Ser Asp Glu	
30	420 425 430	
	gag acc tcc aag tcc tcg cta gag gac aac ttg gca ggg gag gag agc	1701
	Glu Thr Ser Lys Ser Ser Leu Glu Asp Asn Leu Ala Gly Glu Glu Ser	
	435 440 445	
	ccc cag cag ggg gct gaa gcc aag gcg ccc ctg aac atg ggc gag ttc	1749
35	Pro Gln Gln Gly Ala Glu Ala Lys Ala Pro Leu Asn Met Gly Glu Phe	

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	Pro Ser Ser Ser Glu Ser Thr Phe Thr Ser Thr Glu Ser Glu Leu Ser			
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5	gtg cct tac gaa cag ctg atg aat gag tac aac aag gct aac agc ccc			1845
	Val Pro Tyr Glu Gln Leu Met Asn Glu Tyr Asn Lys Ala Asn Ser Pro			
	485	490	495	
	aag ggc aca tgaggcaggg ccggtccccc accccacett tgatgg			1890
	Lys Gly Thr			
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	ggggcagcct cggaactggg agtggggggc caggggcctt cctaaccctc catcatcccc			2010
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	Asp Ser Lys Arg Gly Glu Ala Pro Phe Ala Gln Arg Ile Asp Pro Thr	
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	cgg gag aag ctg aca ccc gag caa ctg cat tcc atg cgg cag gcg gag	149
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	ctt gcc cag tgg cag aag gtc cta cca cgg cgg cga acc cgg aac atc	197
	Leu Ala Gln Trp Gln Lys Val Leu Pro Arg Arg Arg Thr Arg Asn Ile	
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	Val Thr Gly Leu Gly Ile Gly Ala Leu Val Leu Ala Ile Tyr Gly Tyr	
	60 65 70	
	acc ttc tac tcg att tcc cag gag cgt ttc cta gat gag cta gaa gac	293
	Thr Phe Tyr Ser Ile Ser Gln Glu Arg Phe Leu Asp Glu Leu Glu Asp	
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	acagaacttt gcccaactgca cacttgctgt gtacaatgac tgagcccttt cttgtagttt	580
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	Ala Tyr Asn Asn Ile Thr Gly Arg Gln Asp Glu Thr His Phe Thr Val	
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	ttg tca cct tta gca agt ata act gga ata tca cta ttt ttg att ata	257
	Leu Ser Pro Leu Ala Ser Ile Thr Gly Ile Ser Leu Phe Leu Ile Ile	
	40 45 50	
35	tcc atg tgt ctt ctc ttc cta tgg aaa aaa tat caa ccc tac aaa gtt	305

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	Ile Lys Gln Lys Leu Glu Gly Arg Pro Glu Thr Glu Tyr Arg Lys Ala	
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	caa aca ttt tca ggc cat gaa gat gct ctg gat gac ttc gga ata tat	401
	Gln Thr Phe Ser Gly His Glu Asp Ala Leu Asp Asp Phe Gly Ile Tyr	
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	gaa ttt gtt gct ttt cca gat gtt tct ggt gtt tcc agg atc cca agc	449
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	agg tct gtt cca gcc tct gat tgt gta tcg ggg caa gat ttg cac agt	497
	Arg Ser Val Pro Ala Ser Asp Cys Val Ser Gly Gln Asp Leu His Ser	
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	Thr Val Tyr Glu Val Ile Gln His Ile Pro Ala Gln Gln Gln Asp His	
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	Pro Glu	
20		
	attttaagga aaaacagtgg aaaagtatat taatctggaa tcagtgaaga aaccaagacc	660
	aacacctctt actcattatt cctttacatg cagaatagag gcatttatgc aaattgaact	720
	gcagggtttt cagcatatac acaatgtctt gtgcaacaga aaaacatggt ggggaaatat	780
	tctcagtgg agagtgttc tcatgtctgac ggggagaacg aaagtgcag gggtttcctc	840
25	ataagttttg tatgaaatat ctctacaaac ctcaattagt tetactctac actttcacta	900
	tcatcaacac tgagactatc ctgtctcacc tacaatgtg gaaactttac attgttcgat	960
	ttttcagcag actttgtttt attaaatttt tattagtgtt aagaatgcta aagtttcaat	1020
	tttatttcca aatttctatc ttgttatttg tacaacaaag taataaggat ggttgtcaca	1080
	aaaacaaaac tatgccttct cttttttttc aatcaccagt agtatttttg agaagacttg	1140
30	tgaacactta aggaaatgac tattaaagtc ttatttttat ttttttcaag gaaagatgga	1200
	ttcaaataaa ttattctgtt ttgtctttt	1229
	<210> 91	
	<211> 358	
35	<212> PRT	

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<213> Homo sapience

<400> 91

Met Ala Pro Gln Asn Leu Ser Thr Phe Cys Leu Leu Leu Leu Tyr Leu
 5 1 5 10 15
 Ile Gly Ala Val Ile Ala Gly Arg Asp Phe Tyr Lys Ile Leu Gly Val
 20 25 30
 Pro Arg Ser Ala Ser Ile Lys Asp Ile Lys Lys Ala Tyr Arg Lys Leu
 35 40 45
 10 Ala Leu Gln Leu His Pro Asp Arg Asn Pro Asp Asp Pro Gln Ala Gln
 50 55 60
 Glu Lys Phe Gln Asp Leu Gly Ala Ala Tyr Glu Val Leu Ser Asp Ser
 65 70 75 80
 Glu Lys Arg Lys Gln Tyr Asp Thr Tyr Gly Glu Glu Gly Leu Lys Asp
 15 85 90 95
 Gly His Gln Ser Ser His Gly Asp Ile Phe Ser His Phe Phe Gly Asp
 100 105 110
 Phe Gly Phe Met Phe Gly Gly Thr Pro Arg Gln Gln Asp Arg Asn Ile
 115 120 125
 20 Pro Arg Gly Ser Asp Ile Ile Val Asp Leu Glu Val Thr Leu Glu Glu
 130 135 140
 Val Tyr Ala Gly Asn Phe Val Glu Val Val Arg Asn Lys Pro Val Ala
 145 150 155 160
 Arg Gln Ala Pro Gly Lys Arg Lys Cys Asn Cys Arg Gln Glu Met Arg
 25 165 170 175
 Thr Thr Gln Leu Gly Pro Gly Arg Phe Gln Met Thr Gln Glu Val Val
 180 185 190
 Cys Asp Glu Cys Pro Asn Val Lys Leu Val Asn Glu Glu Arg Thr Leu
 195 200 205
 30 Glu Val Glu Ile Glu Pro Gly Val Arg Asp Gly Met Glu Tyr Pro Phe
 210 215 220
 Ile Gly Glu Gly Glu Pro His Val Asp Gly Glu Pro Gly Asp Leu Arg
 225 230 235 240
 Phe Arg Ile Lys Val Val Lys His Pro Ile Phe Glu Arg Arg Gly Asp
 35 245 250 255

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Asp Leu Tyr Thr Asn Val Thr Ile Ser Leu Val Glu Ser Leu Val Gly
 260 265 270
 Phe Glu Met Asp Ile Thr His Leu Asp Gly His Lys Val His Ile Ser
 275 280 285
 5 Arg Asp Lys Ile Thr Arg Pro Gly Ala Lys Leu Trp Lys Lys Gly Glu
 290 295 300
 Gly Leu Pro Asn Phe Asp Asn Asn Asn Ile Lys Gly Ser Leu Ile Ile
 305 310 315 320
 Thr Phe Asp Val Asp Phe Pro Lys Glu Gln Leu Thr Glu Glu Ala Arg
 10 325 330 335
 Glu Gly Ile Lys Gln Leu Leu Lys Gln Gly Ser Val Gln Lys Val Tyr
 340 345 350
 Asn Gly Leu Gln Gly Tyr
 355
 15
 <210> 92
 <211> 226
 <212> PRT
 <213> Homo sapience
 20
 <400> 92
 Met Lys Met Val Ala Pro Trp Thr Arg Phe Tyr Ser Asn Ser Cys Cys
 1 5 10 15
 Leu Cys Cys His Val Arg Thr Gly Thr Ile Leu Leu Gly Val Trp Tyr
 25 20 25 30
 Leu Ile Ile Asn Ala Val Val Leu Leu Ile Leu Leu Ser Ala Leu Ala
 35 40 45
 Asp Pro Asp Gln Tyr Asn Phe Ser Ser Ser Glu Leu Gly Gly Asp Phe
 50 55 60
 30 Glu Phe Met Asp Asp Ala Asn Met Cys Ile Ala Ile Ala Ile Ser Leu
 65 70 75 80
 Leu Met Ile Leu Ile Cys Ala Met Ala Thr Tyr Gly Ala Tyr Lys Gln
 85 90 95
 Arg Ala Ala Trp Ile Ile Pro Phe Phe Cys Tyr Gln Ile Phe Asp Phe
 35 100 105 110

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Ala Leu Asn Met Leu Val Ala Ile Thr Val Leu Ile Tyr Pro Asn Ser
 115 120 125
 Ile Gln Glu Tyr Ile Arg Gln Leu Pro Pro Asn Phe Pro Tyr Arg Asp
 130 135 140
 5 Asp Val Met Ser Val Asn Pro Thr Cys Leu Val Leu Ile Ile Leu Leu
 145 150 155 160
 Phe Ile Ser Ile Ile Leu Thr Phe Lys Gly Tyr Leu Ile Ser Cys Val
 165 170 175
 Trp Asn Cys Tyr Arg Tyr Ile Asn Gly Arg Asn Ser Ser Asp Val Leu
 10 180 185 190
 Val Tyr Val Thr Ser Asn Asp Thr Thr Val Leu Leu Pro Pro Tyr Asp
 195 200 205
 Asp Ala Thr Val Asn Gly Ala Ala Lys Glu Pro Pro Pro Pro Tyr Val
 210 215 220
 15 Ser Ala
 225

 <210> 93
 <211> 195
 20 <212> PRT
 <213> Homo sapience

 <400> 93
 Met Arg Leu Leu Leu Leu Leu Val Ala Ala Ser Ala Met Val Arg
 25 1 5 10 15
 Ser Glu Ala Ser Ala Asn Leu Gly Gly Val Pro Ser Lys Arg Leu Lys
 20 25 30
 Met Gln Tyr Ala Thr Gly Pro Leu Leu Lys Phe Gln Ile Cys Val Ser
 35 40 45
 30 Xaa Gly Tyr Arg Arg Val Phe Glu Glu Tyr Met Arg Val Ile Ser Gln
 50 55 60
 Arg Tyr Pro Asp Ile Arg Ile Glu Gly Glu Asn Tyr Leu Pro Gln Pro
 65 70 75 80
 Ile Tyr Arg His Ile Ala Ser Phe Leu Ser Val Phe Lys Leu Val Leu
 35 85 90 95

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Ile Gly Leu Ile Ile Val Gly Lys Asp Pro Phe Ala Phe Phe Gly Met
 100 105 110
 Gln Ala Pro Ser Ile Trp Gln Trp Gly Gln Glu Asn Lys Val Tyr Ala
 115 120 125
 5 Cys Met Met Val Phe Phe Leu Ser Asn Met Ile Glu Asn Gln Cys Met
 130 135 140
 Ser Thr Gly Ala Phe Glu Ile Thr Leu Asn Asp Val Pro Val Trp Ser
 145 150 155 160
 Lys Leu Glu Ser Gly His Leu Pro Ser Met Gln Gln Leu Val Gln Ile
 10 165 170 175
 Leu Asp Asn Glu Met Lys Leu Asn Val His Met Asp Ser Ile Pro His
 180 185 190
 His Arg Ser
 195
 15
 <210> 94
 <211> 339
 <212> PRT
 <213> Homo sapience
 20
 <400> 94
 Met Asn Trp Glu Leu Leu Leu Trp Leu Leu Val Leu Cys Ala Leu Leu
 1 5 10 15
 Leu Leu Leu Val Gln Leu Leu Arg Phe Leu Arg Ala Asp Gly Asp Leu
 25 20 25 30
 Thr Leu Leu Trp Ala Glu Trp Gln Gly Arg Arg Pro Glu Trp Glu Leu
 35 40 45
 Thr Asp Met Val Val Trp Val Thr Gly Ala Ser Ser Gly Ile Gly Glu
 50 55 60
 30 Glu Leu Ala Tyr Gln Leu Ser Lys Leu Gly Val Ser Leu Val Leu Ser
 65 70 75 80
 Ala Arg Arg Val His Glu Leu Glu Arg Val Lys Arg Arg Cys Leu Glu
 85 90 95
 Asn Gly Asn Leu Lys Glu Lys Asp Ile Leu Val Leu Pro Leu Asp Leu
 35 100 105 110

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Thr Asp Thr Gly Ser His Glu Ala Ala Thr Lys Ala Val Leu Gln Glu
 115 120 125
 Phe Gly Arg Ile Asp Ile Leu Val Asn Asn Gly Gly Met Ser Gln Arg
 130 135 140
 5 Ser Leu Cys Met Asp Thr Ser Leu Asp Val Tyr Arg Lys Leu Ile Glu
 145 150 155 160
 Leu Asn Tyr Leu Gly Thr Val Ser Leu Thr Lys Cys Val Leu Pro His
 165 170 175
 Met Ile Glu Arg Lys Gln Gly Lys Ile Val Thr Val Asn Ser Ile Leu
 10 180 185 190
 Gly Ile Ile Ser Val Pro Leu Ser Ile Gly Tyr Cys Ala Ser Lys His
 195 200 205
 Ala Leu Arg Gly Phe Phe Asn Gly Leu Arg Thr Glu Leu Ala Thr Tyr
 210 215 220
 15 Pro Gly Ile Ile Val Ser Asn Ile Cys Pro Gly Pro Val Gln Ser Asn
 225 230 235 240
 Ile Val Glu Asn Ser Leu Ala Gly Glu Val Thr Lys Thr Ile Gly Asn
 245 250 255
 Asn Gly Asp Gln Ser His Lys Met Thr Thr Ser Arg Cys Val Arg Leu
 20 260 265 270
 Met Leu Ile Ser Met Ala Asn Asp Leu Lys Glu Val Trp Ile Ser Glu
 275 280 285
 Gln Pro Phe Leu Leu Val Thr Tyr Leu Trp Gln Tyr Met Pro Thr Trp
 290 295 300
 25 Ala Trp Trp Ile Thr Asn Lys Met Gly Lys Lys Arg Ile Glu Asn Phe
 305 310 315 320
 Lys Ser Gly Val Asp Ala Asp Ser Ser Tyr Phe Lys Ile Phe Lys Thr
 325 330 335
 Lys His Asp
 30
 <210> 95
 <211> 487
 <212> PRT
 <213> Homo sapience
 35

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<400> 95

Met Asp Gly Thr Glu Thr Arg Gln Arg Arg Leu Asp Ser Cys Gly Lys
 1 5 10 15

Pro Gly Glu Leu Gly Leu Pro His Pro Leu Ser Thr Gly Gly Leu Pro
 5 20 25 30

Val Ala Ser Glu Asp Gly Ala Leu Arg Ala Pro Glu Ser Gln Ser Val
 35 40 45

Thr Pro Lys Pro Leu Glu Thr Glu Pro Ser Arg Glu Thr Ala Trp Ser
 50 55 60

10 Ile Gly Leu Gln Val Thr Val Pro Phe Met Phe Ala Gly Leu Gly Leu
 65 70 75 80

Ser Trp Ala Gly Met Leu Leu Asp Tyr Phe Gln His Trp Pro Val Phe
 85 90 95

Val Glu Val Lys Asp Leu Leu Thr Leu Val Pro Pro Leu Val Gly Leu
 15 100 105 110

Lys Gly Asn Leu Glu Met Thr Leu Ala Ser Arg Leu Ser Thr Ala Ala
 115 120 125

Asn Thr Gly Gln Ile Asp Asp Pro Gln Glu Gln His Arg Val Ile Ser
 130 135 140

20 Ser Asn Leu Ala Leu Ile Gln Val Gln Ala Thr Val Val Gly Leu Leu
 145 150 155 160

Ala Ala Val Ala Ala Leu Leu Leu Gly Val Val Ser Arg Glu Glu Val
 165 170 175

Asp Val Ala Lys Val Glu Leu Leu Cys Ala Ser Ser Val Leu Thr Ala
 25 180 185 190

Phe Leu Ala Ala Phe Ala Leu Gly Val Leu Met Val Cys Ile Val Ile
 195 200 205

Gly Ala Arg Lys Leu Gly Val Asn Pro Asp Asn Ile Ala Thr Pro Ile
 210 215 220

30 Ala Ala Ser Leu Gly Asp Leu Ile Thr Leu Ser Ile Leu Ala Leu Val
 225 230 235 240

Ser Ser Phe Phe Tyr Arg His Lys Asp Ser Arg Tyr Leu Thr Pro Leu
 245 250 255

Val Cys Leu Ser Phe Ala Ala Leu Thr Pro Val Trp Val Leu Ile Ala
 35 260 265 270

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Lys Gln Ser Pro Pro Ile Val Lys Ile Leu Lys Phe Gly Trp Phe Pro
 275 280 285
 Ile Ile Leu Ala Met Val Ile Ser Ser Phe Gly Gly Leu Ile Leu Ser
 290 295 300
 5 Lys Thr Val Ser Lys Gln Gln Tyr Lys Gly Met Ala Ile Phe Thr Pro
 305 310 315 320
 Val Ile Cys Gly Val Gly Gly Asn Leu Val Ala Ile Gln Thr Ser Arg
 325 330 335
 Ile Ser Thr Tyr Leu His Met Trp Ser Ala Pro Gly Val Leu Pro Leu
 10 340 345 350
 Gln Met Lys Lys Phe Trp Pro Asn Pro Cys Ser Thr Phe Cys Thr Ser
 355 360 365
 Glu Ile Asn Ser Met Ser Ala Arg Val Leu Leu Leu Leu Val Val Pro
 370 375 380
 15 Gly His Leu Ile Phe Phe Tyr Ile Ile Tyr Leu Val Glu Gly Gln Ser
 385 390 395 400
 Val Ile Asn Ser Gln Thr Phe Val Val Leu Tyr Leu Leu Ala Gly Leu
 405 410 415
 Ile Gln Val Thr Ile Leu Leu Tyr Leu Ala Glu Val Met Val Arg Leu
 20 420 425 430
 Thr Trp His Gln Ala Leu Asp Pro Asp Asn His Cys Ile Pro Tyr Leu
 435 440 445
 Thr Gly Leu Gly Asp Leu Leu Gly Thr Gly Leu Leu Ala Leu Cys Phe
 450 455 460
 25 Phe Thr Asp Trp Leu Leu Lys Ser Lys Ala Glu Leu Gly Gly Ile Ser
 465 470 475 480
 Glu Leu Ala Ser Gly Pro Pro
 485
 30 <210> 96
 <211> 393
 <212> PRT
 <213> Homo sapience
 35 <400> 96

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Met Arg Thr Leu Phe Asn Leu Leu Trp Leu Ala Leu Ala Cys Ser Pro
 1 5 10 15
 Val His Thr Thr Leu Ser Lys Ser Asp Ala Lys Lys Ala Ala Ser Lys
 20 25 30
 5 Thr Leu Leu Glu Lys Ser Gln Phe Ser Asp Lys Pro Val Gln Asp Arg
 35 40 45
 Gly Leu Val Val Thr Asp Leu Lys Ala Glu Ser Val Val Leu Glu His
 50 55 60
 Arg Ser Tyr Cys Ser Ala Lys Ala Arg Asp Arg His Phe Ala Gly Asp
 10 65 70 75 80
 Val Leu Gly Tyr Val Thr Pro Trp Asn Ser His Gly Tyr Asp Val Thr
 85 90 95
 Lys Val Phe Gly Ser Lys Phe Thr Gln Ile Ser Pro Val Trp Leu Gln
 100 105 110
 15 Leu Lys Arg Arg Gly Arg Glu Met Phe Glu Val Thr Gly Leu His Asp
 115 120 125
 Val Asp Gln Gly Trp Met Arg Ala Val Arg Lys His Ala Lys Gly Leu
 130 135 140
 His Ile Val Pro Arg Leu Leu Phe Glu Asp Trp Thr Tyr Asp Asp Phe
 20 145 150 155 160
 Arg Asn Val Leu Asp Ser Glu Asp Glu Ile Glu Glu Leu Ser Lys Thr
 165 170 175
 Val Val Gln Val Ala Lys Asn Gln His Phe Asp Gly Phe Val Val Glu
 180 185 190
 25 Val Trp Asn Gln Leu Leu Ser Gln Lys Arg Val Gly Leu Ile His Met
 195 200 205
 Leu Thr His Leu Ala Glu Ala Leu His Gln Ala Arg Leu Leu Ala Leu
 210 215 220
 Leu Val Ile Pro Pro Ala Ile Thr Pro Gly Thr Asp Gln Leu Gly Met
 30 225 230 235 240
 Phe Thr His Lys Glu Phe Glu Gln Leu Ala Pro Val Leu Asp Gly Phe
 245 250 255
 Ser Leu Met Thr Tyr Asp Tyr Ser Thr Ala His Gln Pro Gly Pro Asn
 260 265 270
 35 Ala Pro Leu Ser Trp Val Arg Ala Cys Val Gln Val Leu Asp Pro Lys

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275 280 285
 Ser Lys Trp Arg Ser Lys Ile Leu Leu Gly Leu Asn Phe Tyr Gly Met
 290 295 300
 Asp Tyr Ala Thr Ser Lys Asp Ala Arg Glu Pro Val Val Gly Ala Arg
 5 305 310 315 320
 Tyr Ile Gln Thr Leu Lys Asp His Arg Pro Arg Met Val Trp Asp Ser
 325 330 335
 Gln Ala Ser Glu His Phe Phe Glu Tyr Lys Lys Ser Arg Ser Gly Arg
 340 345 350
 10 His Val Val Phe Tyr Pro Thr Leu Lys Ser Leu Gln Val Arg Leu Glu
 355 360 365
 Leu Ala Arg Glu Leu Gly Val Gly Val Ser Ile Trp Glu Leu Gly Gln
 370 375 380
 Gly Leu Asp Tyr Phe Tyr Asp Leu Leu
 15 385 390

 <210> 97
 <211> 196
 <212> PRT
 20 <213> Homo sapience

 <400> 97
 Met Trp Arg Val Pro Gly Thr Thr Arg Arg Pro Val Thr Gly Glu Ser
 1 5 10 15
 25 Pro Gly Met His Arg Pro Glu Ala Met Leu Leu Leu Leu Thr Leu Ala
 20 25 30
 Leu Leu Gly Gly Pro Thr Trp Ala Gly Lys Met Tyr Gly Pro Gly Gly
 35 40 45
 Gly Lys Tyr Phe Ser Thr Thr Glu Asp Tyr Asp His Glu Ile Thr Gly
 30 50 55 60
 Leu Arg Val Ser Val Gly Leu Leu Leu Val Lys Ser Val Gln Val Lys
 65 70 75 80
 Leu Gly Asp Ser Trp Asp Val Lys Leu Gly Ala Leu Gly Gly Asn Thr
 85 90 95
 35 Gln Glu Val Thr Leu Gln Pro Gly Glu Tyr Ile Thr Lys Val Phe Val

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100 105 110
 Ala Phe Gln Ala Phe Leu Arg Gly Met Val Met Tyr Thr Ser Lys Asp
 115 120 125
 Arg Tyr Phe Tyr Phe Gly Lys Leu Asp Gly Gln Ile Ser Ser Ala Tyr
 5 130 135 140
 Pro Ser Gln Glu Gly Gln Val Leu Val Gly Ile Tyr Gly Gln Tyr Gln
 145 150 155 160
 Leu Leu Gly Ile Lys Ser Ile Gly Phe Glu Trp Asn Tyr Pro Leu Glu
 165 170 175
 10 Glu Pro Thr Thr Glu Pro Pro Val Asn Leu Thr Tyr Ser Ala Asn Ser
 180 185 190
 Pro Val Gly Arg
 195
 15 <210> 98
 <211> 107
 <212> PRT
 <213> Homo sapience
 20 <400> 98
 Met Glu Gln Lys Leu Val Glu Glu Ile Leu Gln Ala Ile Thr Met Ser
 1 5 10 15
 Thr Asp Thr Gly Val Ser Leu Pro Ser Tyr Glu Glu Asp Gln Gly Ser
 20 25 30
 25 Lys Leu Ile Arg Lys Ala Lys Glu Ala Pro Phe Val Pro Val Gly Ile
 35 40 45
 Ala Gly Phe Ala Ala Ile Val Ala Tyr Gly Leu Tyr Lys Leu Lys Ser
 50 55 60
 Arg Gly Asn Thr Lys Met Ser Ile His Leu Ile His Met Arg Val Ala
 30 65 70 75 80
 Ala Glu Gly Phe Val Val Gly Ala Met Thr Val Gly Met Gly Tyr Ser
 85 90 95
 Met Tyr Arg Glu Phe Trp Ala Lys Pro Lys Pro
 100 105
 35

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<210> 99

<211> 350

<212> PRT

<213> Homo sapience

5

<400> 99

Met Ser Glu Val Lys Ser Arg Lys Lys Ser Gly Pro Lys Gly Ala Pro

1 5 10 15

Ala Ala Glu Pro Gly Lys Arg Ser Glu Gly Gly Lys Thr Pro Val Ala

10 20 25 30

Arg Ser Ser Gly Gly Gly Gly Trp Ala Asp Pro Arg Thr Cys Leu Ser

35 40 45

Leu Leu Ser Leu Gly Thr Cys Leu Gly Leu Ala Trp Phe Val Phe Gln

50 55 60

15 Gln Ser Glu Lys Phe Ala Lys Val Glu Asn Gln Tyr Gln Leu Leu Lys

65 70 75 80

Leu Glu Thr Asn Glu Phe Gln Gln Leu Gln Ser Lys Ile Ser Leu Ile

85 90 95

Ser Glu Lys Trp Gln Lys Ser Glu Ala Ile Met Glu Gln Leu Lys Ser

20 100 105 110

Phe Gln Ile Ile Ala His Leu Lys Arg Leu Gln Glu Glu Ile Asn Glu

115 120 125

Val Lys Thr Trp Ser Asn Arg Ile Thr Glu Lys Gln Asp Ile Leu Asn

130 135 140

25 Asn Ser Leu Thr Thr Leu Ser Gln Asp Ile Thr Lys Val Asp Gln Ser

145 150 155 160

Thr Thr Ser Met Ala Lys Asp Val Gly Leu Lys Ile Thr Ser Val Lys

165 170 175

Thr Asp Ile Arg Arg Ile Ser Gly Leu Val Thr Asp Val Ile Ser Leu

30 180 185 190

Thr Asp Ser Val Gln Glu Leu Glu Asn Lys Ile Glu Lys Val Glu Lys

195 200 205

Asn Thr Val Lys Asn Ile Gly Asp Leu Leu Ser Ser Ser Ile Asp Arg

210 215 220

35 Thr Ala Thr Leu Arg Lys Thr Ala Ser Glu Asn Ser Gln Arg Ile Asn

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225 230 235 240
 Ser Val Lys Lys Thr Leu Thr Glu Leu Lys Ser Asp Phe Asp Lys His
 245 250 255
 Thr Asp Arg Phe Leu Ser Leu Glu Gly Asp Arg Ala Lys Val Leu Lys
 5 260 265 270
 Thr Val Thr Phe Ala Asn Asp Leu Lys Pro Lys Val Tyr Asn Leu Lys
 275 280 285
 Lys Asp Phe Ser Arg Leu Glu Pro Leu Val Asn Asp Leu Thr Leu Arg
 290 295 300
 10 Ile Gly Arg Leu Val Thr Asp Leu Leu Gln Arg Glu Lys Glu Ile Ala
 305 310 315 320
 Phe Leu Ser Glu Lys Ile Ser Asn Leu Thr Ile Val Gln Ala Glu Ile
 325 330 335
 Lys Asp Ile Lys Asp Glu Ile Ala His Ile Ser Asp Met Asn
 15 340 345 350

 <210> 100
 <211> 107
 <212> PRT
 20 <213> Homo sapience

 <400> 100
 Met Ser Ser Ala Gly Thr Ala Thr Pro Leu Glu Met Asp His Lys Leu
 1 5 10 15
 25 Thr Ser Gln Pro Gly Arg Pro Ser Phe Tyr Cys Asn Ser Arg His Ser
 20 25 30
 Ile Val Gly Ser Ser His Gln Leu Gly Phe Trp Phe Ser His Leu Glu
 35 40 45
 Ser Ser Gly Leu Lys Val Phe Gln Val Ser Leu Pro Cys Glu Cys Val
 30 50 55 60
 Asn Leu Pro Thr Arg Ile Ala Ser Val Val Leu Ser Leu Met Ser Leu
 65 70 75 80
 Leu Val Val Gly Gln Ala Pro Ala Trp Glu Gly Ser Leu Leu Arg Gly
 85 90 95
 35 Arg Pro Ala Gly Gly Ala His Leu Cys Ala Ala

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100

105

<210> 101

<211> 1074

5

<212> DNA

<213> Homo Sapience

<400> 101

10

atggctccgc agaacctgag caccttttgc ctgttgctgc tatacctcat cggggcggtg 60

attgccggac gagatttcta taagatcttg ggggtgcctc gaagtgcctc tataaaggat 120

attaaaaagg cctataggaa actagccctg cagcttcac cgcaccggaa ccctgatgat 180

ccacaagccc aggagaaatt ccaggatctg ggtgctgctt atgaggttct gtcagatagt 240

gagaaacgga aacagtacga tacttatggt gaagaaggat taaaagatgg tcatcagagc 300

tcccatggag acattttttc acacttcttt ggggattttg gtttcatgtt tggaggaacc 360

15

cctcgtcagc aagacagaaa tattccaaga ggaagtgata ttattgtaga tctagaagtc 420

actttggaag aagtatatgc aggaaathtt gtggaagtag ttagaaacaa acctgtggca 480

aggcaggtc ctggcaaacg gaagtgaat tgctggcaag agatgcggac caccagctg 540

ggccctgggc gcttccaaat gaccaggag gtggtctgcg acgaatgcc taatgtcaaa 600

ctagtgaatg aagaacgaac gctggaagta gaaatagagc ctggggtgag agacggcatg 660

20

gagtaccctt ttattggaga aggtgagcct cacgtggatg gggagcctgg agatttacgg 720

ttccgaatca aagttgtcaa gcaccaata ttgaaagga gaggagatga tttgtacaca 780

aatgtgacaa tctcattagt tgagtcactg gttggctttg agatggatat tactcacttg 840

gatggtcaca aggtacatat ttccgggat aagatcacca ggccaggagc gaagctatgg 900

aagaaagggg aagggtccc caactttgac aacaacaata tcaagggctc tttgataatc 960

25

acttttgatg tggattttcc aaaagaacag ttaacagagg aagcgagaga aggtatcaaa 1020

cagctactga aacaagggtc agtgcagaag gtatacaatg gactgcaagg atat 1074

<210> 102

<211> 678

30

<212> DNA

<213> Homo Sapience

<400> 102

35

atgaagatgg tcgcgcctg gacgcggttc tactccaaca gctgctgctt gtgctgccat 60

gtccgcaccg gcaccatcct gctcggcgtc tggatatga tcatcaatgc tgtggtactg 120

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5 ttgattttat tgagtgcct ggctgatccg gatcagtata acttttcaag ttctgaactg 180
 ggaggtgact ttgagttcat ggatgatgcc aacatgtgca ttgccattgc gattttctett 240
 ctcatgatcc tgatatgtgc tatggctact tacggagcgt acaagcaacg cgcagcctgg 300
 atcatcccat tcttctgtta ccagatcttt gaactttgcc tgaacatggt ggttgcaatc 360
 10 actgtgctta tttatccaaa ctccattcag gaatacatac ggcaactgcc tcctaatttt 420
 ccctacagag atgatgtcat gtcagtgaat cctacctgtt tggtccttat tattcttctg 480
 tttattagca ttatcttgac ttttaagggg tacttgatta gctgtgtttg gaactgctac 540
 cgatacatca atggtaggaa ctctctgat gtcttggttt atgttaccag caatgacact 600
 acggtgctgc taccctcgta tgatgatgcc actgtgaatg gtgctgccaa ggagccaccg 660
 15 ccaccttacg tgtctgcc 678

<210> 103

<211> 585

<212> DNA

15 <213> Homo Sapience

<400> 103

20 atgaggett c tgetgettct cctagtggcg gegtctgcga tggtcgggag cgaggcctcg 60
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 ctcaagttcc agatttgtgt ttcttgaggt tataggcggg tgtttgagga gtacatgcgg 180
 gttattagcc agcggtagcc agacatccgc attgaaggag agaattacct cctcaacca 240
 atatatagac acatagcatc ttctctgtca gtcttcaaac tagtattaat aggetttaata 300
 attgttggca aggatccttt tgccttcttt ggcatgcaag ctcttagcat ctggcagtg 360
 ggccaagaaa ataaggttta tgcattgtat atggttttct tcttgagcaa catgattgag 420
 25 aaccagtgt tgtcaacagg tgcatttgag ataacttta atgatgtacc tgtgtggtct 480
 aagctggaat ctggtcacct tccatccatg caacaacttg ttcaaattct tgacaatgaa 540
 atgaagctca atgtgcatat ggattcaatc ccacaccatc gatca 585

<210> 104

30 <211> 1017

<212> DNA

<213> Homo Sapience

<400> 104

35 atgaactggg agctgctgct gtggctgctg gtgctgtgcg cgctgctcct gctcttggtg 60

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	cagctgctgc gcttcctgag ggctgacggc gacctgacgc tactatgggc cgagtggcag	120
	ggacgacgcc cagaatggga gctgactgat atggtggtgt gggtagctgg agcctcgagt	180
	ggaattggtg aggagctggc ttaccagttg tctaaactag gagtttctct tgtgctgtca	240
	gccagaagag tgcattgagct ggaaagggtg aaaagaagat gcctagagaa tggcaattta	300
5	aaagaaaaag atatacttgt tttgcccctt gacctgaccg aacttggttc ccatgaagcg	360
	gctaccaaag ctgttctcca ggagtttggg agaatcgaca ttctggtcaa caatggtgga	420
	atgtcccagc gttctctgtg catggatacc agcttggtatg tctacagaaa gctaatagag	480
	cttaactact tagggacggt gtccttgaca aaatgtgttc tgccctcacat gatcgagagg	540
	aagcaaggaa agattgttac tgtgaatagc atcctgggta tcatatctgt acctctttcc	600
10	attggatact gtgctagcaa gcatgctctc cggggttttt ttaatggcct tcgaacagaa	660
	cttgccacat acccaggtat aatagtttct aacatttgcc caggacctgt gcaatcaa	720
	attgtggaga attccctagc tggagaagtc acaaagacta taggcaataa tggagaccag	780
	tcccacaaga tgacaaccag tcgttgtgtg cggtgatgt taatcagcat ggccaatgat	840
	ttgaaagaag tttggatctc agaacaacct ttcttggttag taacatattt gtggcaatac	900
15	atgccaaacct gggcctggtg gataaccaac aagatgggga agaaaaggat tgagaacttt	960
	aagagtgggtg tggatgcaga ctcttcttat tttaaaatct ttaagacaaa acatgac	1017
	<210> 105	
	<211> 1461	
20	<212> DNA	
	<213> Homo Sapience	
	<400> 105	
	atggatggga cagagacccg gcagcggagg ctggacagct gtggcaagcc aggggagctg	60
25	gggcttctc accccctcag cacaggagga ctccctgtag cctcagaaga tggagctctc	120
	agggccccctg agagccaaag cgtgaccccc aagccactgg agactgagcc tagcagggag	180
	accgctggt ccataggcct tcagggtgacc gtgcccttca tgtttgcagg cctgggactg	240
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	gtggagttgc tgtgtgccag cagtgtctc actgccttcc ttgcagcctt tgccctgggg	600
	gtgctgatgg tctgtatagt gattggtgct cgaaagctcg gggtaaccc agacaacatt	660
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	gtcataaaca gccagacctt tgtggtgctc tacctgctgg caggcctgat ccaggtgaca	1260
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	tcagataagc cgggtcaaga cgggggtttg gtggtgacgg acctcaaagc tgagagtgtg	180
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	aagcgcgtgg gcctcatcca catgctcacc cacttggccg aggctctgca ccagggccgg	660
	ctgctggccc tcctggteat cccgcctgcc atcaccccg ggaccgacca gctgggcatg	720
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	cactttctcg agtacaagaa gagccgcagt gggaggcacg tcgtcttcta cccaacctg	1080
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	ctccttggca tcaagagcat tggctttgaa tggaattatc cactagagga gccgaccact	540
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	gcaccattcg taccgcttgg aatagcgggt tttgcagcaa ttgttgcata tggattatat	180
	aaactgaaga gcaggggaaa tactaaaatg tccattcattc tgatccacat gcgtgtggca	240
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<210> 109

<211> 1050

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	ctagaaacca atgaattcca acaacttcaa agtaaaatca gtttaatttc agaaaagtgg	300
	cagaaatctg aagctatcat ggaacaattg aagtcttttc aaataattgc tcatctaaa	360
	cgtctacagg aagaaattaa tgaggtaaaa acttggtcca ataggataac tgaaaaacag	420
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	aaaccaaagg tgtataatct aaagaaggac ttttccggt tagaaccatt agtaaattgat	900
	ttaacactac gcattgggag attgggtacc gacttactac aaagagagaa agaaattgct	960
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<211> 321

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35	ggtttttggg ttagtcatct agagtcgtct ggactaaagg totttcaggt ctcttgccc	180

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 gaggagtgtg tggaacagga cccgggacag aggaacc atg gct ccg cag aac ctg 175
 Met Ala Pro Gln Asn Leu
 1 5
 20 agc acc ttt tgc ctg ttg ctg cta tac ctc atc ggg gcg gtg att gcc 223
 Ser Thr Phe Cys Leu Leu Leu Leu Tyr Leu Ile Gly Ala Val Ile Ala
 10 15 20
 gga cga gat ttc tat aag atc ttg ggg gtg cct cga agt gcc tct ata 271
 Gly Arg Asp Phe Tyr Lys Ile Leu Gly Val Pro Arg Ser Ala Ser Ile
 25 30 35
 25 aag gat att aaa aag gcc tat agg aaa cta gcc ctg cag ctt cat ccc 319
 Lys Asp Ile Lys Lys Ala Tyr Arg Lys Leu Ala Leu Gln Leu His Pro
 40 45 50
 gac cgg aac cct gat gat cca caa gcc cag gag aaa ttc cag gat ctg 367
 Asp Arg Asn Pro Asp Asp Pro Gln Ala Gln Glu Lys Phe Gln Asp Leu
 30 55 60 65 70
 ggt gct gct tat gag gtt ctg tca gat agt gag aaa cgg aaa cag tac 415
 Gly Ala Ala Tyr Glu Val Leu Ser Asp Ser Glu Lys Arg Lys Gln Tyr
 75 80 85
 gat act tat ggt gaa gaa gga tta aaa gat ggt cat cag agc tcc cat 463
 35 Asp Thr Tyr Gly Glu Glu Gly Leu Lys Asp Gly His Gln Ser Ser His

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5	gga acc cct cgt cag caa gac aga aat att cca aga gga agt gat att			559
	Gly Thr Pro Arg Gln Gln Asp Arg Asn Ile Pro Arg Gly Ser Asp Ile			
	120	125	130	
	att gta gat cta gaa gtc act ttg gaa gaa gta tat gca gga aat ttt			607
	Ile Val Asp Leu Glu Val Thr Leu Glu Glu Val Tyr Ala Gly Asn Phe			
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	Val Glu Val Val Arg Asn Lys Pro Val Ala Arg Gln Ala Pro Gly Lys			
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	cgg aag tgc aat tgt cgg caa gag atg cgg acc acc cag ctg ggc cct			703
15	Arg Lys Cys Asn Cys Arg Gln Glu Met Arg Thr Thr Gln Leu Gly Pro			
	170	175	180	
	ggg cgc ttc caa atg acc cag gag gtg gtc tgc gac gaa tgc cct aat			751
	Gly Arg Phe Gln Met Thr Gln Glu Val Val Cys Asp Glu Cys Pro Asn			
	185	190	195	
20	gtc aaa cta gtg aat gaa gaa cga acg ctg gaa gta gaa ata gag cct			799
	Val Lys Leu Val Asn Glu Glu Arg Thr Leu Glu Val Glu Ile Glu Pro			
	200	205	210	
	ggg gtg aga gac ggc atg gag tac ccc ttt att gga gaa ggt gag cct			847
	Gly Val Arg Asp Gly Met Glu Tyr Pro Phe Ile Gly Glu Gly Glu Pro			
25	215	220	225	230
	cac gtg gat ggg gag cct gga gat tta cgg ttc cga atc aaa gtt gtc			895
	His Val Asp Gly Glu Pro Gly Asp Leu Arg Phe Arg Ile Lys Val Val			
	235	240	245	
	aag cac cca ata ttt gaa agg aga gga gat gat ttg tac aca aat gtg			943
30	Lys His Pro Ile Phe Glu Arg Arg Gly Asp Asp Leu Tyr Thr Asn Val			
	250	255	260	
	aca atc tca tta gtt gag tca ctg gtt ggc ttt gag atg gat att act			991
	Thr Ile Ser Leu Val Glu Ser Leu Val Gly Phe Glu Met Asp Ile Thr			
	265	270	275	
35	cac ttg gat ggt cac aag gta cat att tcc cgg gat aag atc acc agg			1039

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	His Leu Asp Gly His Lys Val His Ile Ser Arg Asp Lys Ile Thr Arg	
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	cca gga gcg aag cta tgg aag aaa ggg gaa ggg ctc ccc aac ttt gac	1087
	Pro Gly Ala Lys Leu Trp Lys Lys Gly Glu Gly Leu Pro Asn Phe Asp	
5	295 300 305 310	
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	Asn Asn Asn Ile Lys Gly Ser Leu Ile Ile Thr Phe Asp Val Asp Phe	
	315 320 325	
	cca aaa gaa cag tta aca gag gaa gcg aga gaa ggt atc aaa cag cta	1183
10	Pro Lys Glu Gln Leu Thr Glu Glu Ala Arg Glu Gly Ile Lys Gln Leu	
	330 335 340	
	ctg aaa caa ggg tca gtg cag aag gta tac aat gga ctg caa gga tat	1231
	Leu Lys Gln Gly Ser Val Gln Lys Val Tyr Asn Gly Leu Gln Gly Tyr	
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	gcggggcgac gggcgagcgg gccgggagcc ggagcggcgg aggagccggc agcagcggcg	180
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	Gly Val Trp Tyr Leu Ile Ile Asn Ala Val Val Leu Leu Ile Leu Leu	
	30 35 40	
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	Ser Ala Leu Ala Asp Pro Asp Gln Tyr Asn Phe Ser Ser Ser Glu Leu	
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	gga ggt gac ttt gag ttc atg gat gat gcc aac atg tgc att gcc att	481
	Gly Gly Asp Phe Glu Phe Met Asp Asp Ala Asn Met Cys Ile Ala Ile	
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	Ala Ile Ser Leu Leu Met Ile Leu Ile Cys Ala Met Ala Thr Tyr Gly	
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20	Ala Tyr Lys Gln Arg Ala Ala Trp Ile Ile Pro Phe Phe Cys Tyr Gln	
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	atc ttt gac ttt gcc ctg aac atg ttg gtt gca atc act gtg ctt att	625
	Ile Phe Asp Phe Ala Leu Asn Met Leu Val Ala Ile Thr Val Leu Ile	
	110 115 120	
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	Tyr Pro Asn Ser Ile Gln Glu Tyr Ile Arg Gln Leu Pro Pro Asn Phe	
	125 130 135 140	
	ccc tac aga gat gat gtc atg tca gtg aat cct acc tgt ttg gtc ctt	721
	Pro Tyr Arg Asp Asp Val Met Ser Val Asn Pro Thr Cys Leu Val Leu	
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	att att ctt ctg ttt att agc att atc ttg act ttt aag ggt tac ttg	769
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	160 165 170	
	att agc tgt gtt tgg aac tgc tac cga tac atc aat ggt agg aac tcc	817
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	190	195	200	
5	ccc ccg tat gat gat gcc act gtg aat ggt gct gcc aag gag cca ccg			913
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	Pro Pro Tyr Val Ser Ala			
10	225			
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<221> CDS

<222> (43)...(630)

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                                     . 1

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Leu Leu Leu Leu Val Ala Ala Ser Ala Met Val Arg Ser Glu Ala Ser

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   gcc aat ctg ggc ggc gtg ccc agc aag aga tta aag atg cag tac gcc      150
Ala Asn Leu Gly Gly Val Pro Ser Lys Arg Leu Lys Met Gln Tyr Ala
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   acg ggg ccg ctg ctc aag ttc cag att tgt gtt tcc tga ggt tat agg      198
15   Thr Gly Pro Leu Leu Lys Phe Gln Ile Cys Val Ser Xaa Gly Tyr Arg
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   cgg gtg ttt gag gag tac atg cgg gtt att agc cag cgg tac cca gac      246
Arg Val Phe Glu Glu Tyr Met Arg Val Ile Ser Gln Arg Tyr Pro Asp
               55           60           65
20   atc cgc att gaa gga gag aat tac ctc cct caa cca ata tat aga cac      294
Ile Arg Ile Glu Gly Glu Asn Tyr Leu Pro Gln Pro Ile Tyr Arg His
               70           75           80
   ata gca tct ttc ctg tca gtc ttc aaa cta gta tta ata ggc tta ata      342
Ile Ala Ser Phe Leu Ser Val Phe Lys Leu Val Leu Ile Gly Leu Ile

25   85           90           95           100
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Ile Val Gly Lys Asp Pro Phe Ala Phe Phe Gly Met Gln Ala Pro Ser
               105           110           115
   atc tgg cag tgg ggc caa gaa aat aag gtt tat gca tgt atg atg gtt      438
30   Ile Trp Gln Trp Gly Gln Glu Asn Lys Val Tyr Ala Cys Met Met Val
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Phe Phe Leu Ser Asn Met Ile Glu Asn Gln Cys Met Ser Thr Gly Ala
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35   ttt gag ata act tta aat gat gta cct gtg tgg tct aag ctg gaa tct      534

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	Gly His Leu Pro Ser Met Gln Gln Leu Val Gln Ile Leu Asp Asn Glu	
5	165 170 175 180	
	atg aag ctc aat gtg cat atg gat tca atc cca cac cat cga tca	627
	Met Lys Leu Asn Val His Met Asp Ser Ile Pro His His Arg Ser	
	185 190 195	
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	agatgctttc ttggcaggct cgttgtacct cttggaaaac ctcaatgcaa gatagtgttt	800
	cagtgtggc atattttgga attctgcaca ttcattggagt gcaataatac tgtatagctt	860
	tccccacctc ccacaaaatc acccagttaa tgttgtgtgtg tgtttttttt tttaaggtaa	920
	acattactac ttgtaacttt ttttcttagt catatttgaa aaagtagaaa attgagttac	980
15	aatttgattt tttttccaaa gatgtctgtt aaatctgttg tgcttttata tgaatatttg	1040
	ttttttatag tttaaaattg atcctttggg aatccagttg aagttcccaa atactttata	1100
	agagtttatc agacatctct aatttggtcca tgtccagttt atacagttta caaaatatag	1160
	cagatgcaag attatggggg aaatcctata ttcagagtac tctataaatt tttgtgtatg	1220
	tgtgtatgtg cgtgtgatta ccagagaact actaaaaaaaa ccaactgctt tttaaatcct	1280
20	attgtgtagt taaagtgtca tgccttgacc aatctaataga attgattaat taactgggcc	1340
	tttatactta actaaataaa aaactaagca gatatgagtt	1380
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	gactctgggtg cgggcgctct tcttcccccc gagctggggc tgcgcggccg ca atg aac	118
	Met Asn	
35	1	

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	tgg gag ctg ctg ctg tgg ctg ctg gtg ctg tgc gcg ctg ctc ctg ctc	166
	Trp Glu Leu Leu Leu Trp Leu Leu Val Leu Cys Ala Leu Leu Leu Leu	
	5 10 15	
	ttg gtg cag ctg ctg cgc ttc ctg agg gct gac ggc gac ctg acg cta	214
5	Leu Val Gln Leu Leu Arg Phe Leu Arg Ala Asp Gly Asp Leu Thr Leu	
	20 25 30	
	cta tgg gcc gag tgg cag gga cga cgc cca gaa tgg gag ctg act gat	262
	Leu Trp Ala Glu Trp Gln Gly Arg Arg Pro Glu Trp Glu Leu Thr Asp	
	35 40 45 50	
10	atg gtg gtg tgg gtg act gga gcc tcg agt gga att ggt gag gag ctg	310
	Met Val Val Trp Val Thr Gly Ala Ser Ser Gly Ile Gly Glu Glu Leu	
	55 60 65	
	gct tac cag ttg tct aaa cta gga gtt tct ctt gtg ctg tca gcc aga	358
	Ala Tyr Gln Leu Ser Lys Leu Gly Val Ser Leu Val Leu Ser Ala Arg	
15	70 75 80	
	aga gtg cat gag ctg gaa agg gtg aaa aga aga tgc cta gag aat ggc	406
	Arg Val His Glu Leu Glu Arg Val Lys Arg Arg Cys Leu Glu Asn Gly	
	85 90 95	
	aat tta aaa gaa aaa gat ata ctt gtt ttg ccc ctt gac ctg acc gac	454
20	Asn Leu Lys Glu Lys Asp Ile Leu Val Leu Pro Leu Asp Leu Thr Asp	
	100 105 110	
	act ggt tcc cat gaa gcg gct acc aaa gct gtt ctc cag gag ttt ggt	502
	Thr Gly Ser His Glu Ala Ala Thr Lys Ala Val Leu Gln Glu Phe Gly	
	115 120 125 130	
25	aga atc gac att ctg gtc aac aat ggt gga atg tcc cag cgt tct ctg	550
	Arg Ile Asp Ile Leu Val Asn Asn Gly Gly Met Ser Gln Arg Ser Leu	
	135 140 145	
	tgc atg gat acc agc ttg gat gtc tac aga aag cta ata gag ctt aac	598
	Cys Met Asp Thr Ser Leu Asp Val Tyr Arg Lys Leu Ile Glu Leu Asn	
30	150 155 160	
	tac tta ggg acg gtg tcc ttg aca aaa tgt gtt ctg cct cac atg atc	646
	Tyr Leu Gly Thr Val Ser Leu Thr Lys Cys Val Leu Pro His Met Ile	
	165 170 175	
	gag agg aag caa gga aag att gtt act gtg aat agc atc ctg ggt atc	694
35	Glu Arg Lys Gln Gly Lys Ile Val Thr Val Asn Ser Ile Leu Gly Ile	

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	180	185	190	
	ata tct gta cct ctt tcc att gga tac tgt gct agc aag cat gct ctc			742
	Ile Ser Val Pro Leu Ser Ile Gly Tyr Cys Ala Ser Lys His Ala Leu			
	195	200	205	210
5	cgg ggt ttt ttt aat ggc ctt cga aca gaa ctt gcc aca tac cca ggt			790
	Arg Gly Phe Phe Asn Gly Leu Arg Thr Glu Leu Ala Thr Tyr Pro Gly			
	215	220	225	
	ata ata gtt tct aac att tgc cca gga cct gtg caa tca aat att gtg			838
	Ile Ile Val Ser Asn Ile Cys Pro Gly Pro Val Gln Ser Asn Ile Val			
10	230	235	240	
	gag aat tcc cta gct gga gaa gtc aca aag act ata ggc aat aat gga			886
	Glu Asn Ser Leu Ala Gly Glu Val Thr Lys Thr Ile Gly Asn Asn Gly			
	245	250	255	
	gac cag tcc cac aag atg aca acc agt cgt tgt gtg cgg ctg atg tta			934
15	Asp Gln Ser His Lys Met Thr Thr Ser Arg Cys Val Arg Leu Met Leu			
	260	265	270	
	atc agc atg gcc aat gat ttg aaa gaa gtt tgg atc tca gaa caa cct			982
	Ile Ser Met Ala Asn Asp Leu Lys Glu Val Trp Ile Ser Glu Gln Pro			
	275	280	285	290
20	ttc ttg tta gta aca tat ttg tgg caa tac atg cca acc tgg gcc tgg			1030
	Phe Leu Leu Val Thr Tyr Leu Trp Gln Tyr Met Pro Thr Trp Ala Trp			
	295	300	305	
	tgg ata acc aac aag atg ggg aag aaa agg att gag aac ttt aag agt			1078
	Trp Ile Thr Asn Lys Met Gly Lys Lys Arg Ile Glu Asn Phe Lys Ser			
25	310	315	320	
	ggt gtg gat gca gac tct tct tat ttt aaa atc ttt aag aca aaa cat			1126
	Gly Val Asp Ala Asp Ser Ser Tyr Phe Lys Ile Phe Lys Thr Lys His			
	325	330	335	
	gac tgaaaagagc atctgtactt ttcaagccac tggaggggaaa aatggaaaac a			1180
30	Asp			
	tgaaaacagc aatcttctta tgettctgaa taatcaaaga ctaatttgtg gttttacttt			1240
	ttaatagata tgacttttgc tccaacatgg aatgaaataa aaaataagta at			1292
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 10 atg gat ggg aca gag acc cgg cag cgg agg ctg gac agc tgt ggc aag 103
 Met Asp Gly Thr Glu Thr Arg Gln Arg Arg Leu Asp Ser Cys Gly Lys
 1 5 10 15
 cca ggg gag ctg ggg ctt cct cac ccc ctc agc aca gga gga ctc cct 151
 Pro Gly Glu Leu Gly Leu Pro His Pro Leu Ser Thr Gly Gly Leu Pro
 15 20 25 30
 gta gcc tca gaa gat gga gct ctc agg gcc cct gag agc caa agc gtg 199
 Val Ala Ser Glu Asp Gly Ala Leu Arg Ala Pro Glu Ser Gln Ser Val
 35 40 45
 acc ccc aag cca ctg gag act gag cct agc agg gag acc gcc tgg tcc 247
 20 Thr Pro Lys Pro Leu Glu Thr Glu Pro Ser Arg Glu Thr Ala Trp Ser
 50 55 60
 ata ggc ctt cag gtg acc gtg ccc ttc atg ttt gca ggc ctg gga ctg 295
 Ile Gly Leu Gln Val Thr Val Pro Phe Met Phe Ala Gly Leu Gly Leu
 65 70 75 80
 25 tcc tgg gcc ggc atg ctt ctg gac tat ttc cag cac tgg cct gtg ttt 343
 Ser Trp Ala Gly Met Leu Leu Asp Tyr Phe Gln His Trp Pro Val Phe
 85 90 95
 gtg gag gtg aaa gac ctt ttg aca ttg gtg ccg ccc ctg gtg ggc ctg 391
 Val Glu Val Lys Asp Leu Leu Thr Leu Val Pro Pro Leu Val Gly Leu
 100 105 110
 30 aag ggg aac ctg gag atg aca ctg gca tcc aga ctc tcc aca gct gcc 439
 Lys Gly Asn Leu Glu Met Thr Leu Ala Ser Arg Leu Ser Thr Ala Ala
 115 120 125
 aac act gga caa att gat gac ccc cag gag cag cac aga gtc atc agc 487
 35 Asn Thr Gly Gln Ile Asp Asp Pro Gln Glu Gln His Arg Val Ile Ser

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	130	135	140	
	agc aac ctg gcc ctc atc cag gtg cag gcc act gtc gtg ggg ctc ttg			535
	Ser Asn Leu Ala Leu Ile Gln Val Gln Ala Thr Val Val Gly Leu Leu			
	145	150	155	160
5	gct gct gtg gct gcg ctg ctg ttg ggc gtg gtg tct cga gag gaa gtg			583
	Ala Ala Val Ala Ala Leu Leu Leu Gly Val Val Ser Arg Glu Glu Val			
	165	170	175	
	gat gtc gcc aag gtg gag ttg ctg tgt gcc agc agt gtc ctc act gcc			631
	Asp Val Ala Lys Val Glu Leu Leu Cys Ala Ser Ser Val Leu Thr Ala			
10	180	185	190	
	ttc ctt gca gcc ttt gcc ctg ggg gtg ctg atg gtc tgt ata gtg att			679
	Phe Leu Ala Ala Phe Ala Leu Gly Val Leu Met Val Cys Ile Val Ile			
	195	200	205	
	ggc gct cga aag ctc ggg gtc aac cca gac aac att gcc acg ccc att			727
15	Gly Ala Arg Lys Leu Gly Val Asn Pro Asp Asn Ile Ala Thr Pro Ile			
	210	215	220	
	gca gcc agc ctg gga gac ctc atc aca ctg tcc att ctg gct ttg gtt			775
	Ala Ala Ser Leu Gly Asp Leu Ile Thr Leu Ser Ile Leu Ala Leu Val			
	225	230	235	240
20	agc agc ttc ttc tac aga cac aaa gat agt cgg tat ctg acg ccg ctg			823
	Ser Ser Phe Phe Tyr Arg His Lys Asp Ser Arg Tyr Leu Thr Pro Leu			
	245	250	255	
	gtc tgc ctc agc ttt gcg gct ctg acc cca gtg tgg gtc ctc att gcc			871
	Val Cys Leu Ser Phe Ala Ala Leu Thr Pro Val Trp Val Leu Ile Ala			
25	260	265	270	
	aag cag agc cca ccc atc gtg aag atc ctg aag ttt ggc tgg ttc cca			919
	Lys Gln Ser Pro Pro Ile Val Lys Ile Leu Lys Phe Gly Trp Phe Pro			
	275	280	285	
	atc atc ctg gcc atg gtc atc agc agt ttc gga gga ctc atc ttg agc			967
30	Ile Ile Leu Ala Met Val Ile Ser Ser Phe Gly Gly Leu Ile Leu Ser			
	290	295	300	
	aaa acc gtt tct aaa cag cag tac aaa ggc atg gcg ata ttt acc ccc			1015
	Lys Thr Val Ser Lys Gln Gln Tyr Lys Gly Met Ala Ile Phe Thr Pro			
	305	310	315	320
35	gtc ata tgt ggt gtt ggt ggc aat ctg gtg gcc att cag acc agc cga			1063

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	Val Ile Cys Gly Val Gly Gly Asn Leu Val Ala Ile Gln Thr Ser Arg	
	325 330 335	
	atc tca acc tac ctg cac atg tgg agt gca cct ggc gtc ctg ccc ctc	1111
	Ile Ser Thr Tyr Leu His Met Trp Ser Ala Pro Gly Val Leu Pro Leu	
5	340 345 350	
	cag atg aag aaa ttc tgg ccc aac ccg tgt tct act ttc tgc acg tca	1159
	Gln Met Lys Lys Phe Trp Pro Asn Pro Cys Ser Thr Phe Cys Thr Ser	
	355 360 365	
	gaa atc aat tcc atg tca gct cga gtc ctg ctc ttg ctg gtg gtc cca	1207
10	Glu Ile Asn Ser Met Ser Ala Arg Val Leu Leu Leu Leu Val Val Pro	
	370 375 380	
	ggc cat ctg att ttc ttc tac atc atc tac ctg gtg gag ggt cag tca	1255
	Gly His Leu Ile Phe Phe Tyr Ile Ile Tyr Leu Val Glu Gly Gln Ser	
	385 390 395 400	
15	gtc ata aac agc cag acc ttt gtg gtg ctc tac ctg ctg gca ggc ctg	1303
	Val Ile Asn Ser Gln Thr Phe Val Val Leu Tyr Leu Leu Ala Gly Leu	
	405 410 415	
	atc cag gtg aca atc ctg ctg tac ctg gca gaa gtg atg gtt cgg ctg	1351
	Ile Gln Val Thr Ile Leu Leu Tyr Leu Ala Glu Val Met Val Arg Leu	
20	420 425 430	
	act tgg cac cag gcc ctg gat cct gac aac cac tgc atc ccc tac ctt	1399
	Thr Trp His Gln Ala Leu Asp Pro Asp Asn His Cys Ile Pro Tyr Leu	
	435 440 445	
	aca ggg ctg ggg gac ctg ctc ggt act ggc ctc ctg gca ctc tgc ttt	1447
25	Thr Gly Leu Gly Asp Leu Leu Gly Thr Gly Leu Leu Ala Leu Cys Phe	
	450 455 460	
	ttc act gac tgg cta ctg aag agc aag gca gag ctg ggt ggc atc tca	1495
	Phe Thr Asp Trp Leu Leu Lys Ser Lys Ala Glu Leu Gly Gly Ile Ser	
	465 470 475 480	
30	gaa ctg gca tct gga cct ccc taactgggcc ccgctgggtcc catttgetca ttag	1550
	Glu Leu Ala Ser Gly Pro Pro	
	485	
	aatttcctct cacatcagtg ggatacagaa ttcagttttet cccttgccag gtccttgggga	1610
	tgggtgaccc ctgcctctgc agtagccttt tgtgagttctg ctaaggtagc tctcacacac	1670
35	ctcggctctg ggggtgatac ctgagcctgc aatagagccc tgaaatcaag agcatggctt	1730

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gagtgtgtga atatgatgtg tgcacatgct taatgagcgt gcaagtgtgc acacgtttgt 1790
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 ggggtgtgtt gctcttttcc atgcccagc aaccagatt ggggtggagc aggaaggagc 1910
 tcttttctgt tccaagcct cagaactctt gagctgtggc ttacttgctg tcttcaccag 1970
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 ggggcctcat acaacccttc atctgcactc aacatttaat cgtgtccttg ctgtcttttt 2090
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 20 cctactgtga cacacctaac atg cgg aca ctc ttc aac ctc ctc tgg ctt 110
 Met Arg Thr Leu Phe Asn Leu Leu Trp Leu
 1 5 10
 gcc ctg gcc tgc agc cct gtt cac act acc ctg tca aag tca gat gcc 158
 Ala Leu Ala Cys Ser Pro Val His Thr Thr Leu Ser Lys Ser Asp Ala
 25 15 20 25
 aaa aaa gcc gcc tca aag acg ctg ctg gag aag agt cag ttt tca gat 203
 Lys Lys Ala Ala Ser Lys Thr Leu Leu Glu Lys Ser Gln Phe Ser Asp
 30 30 35 40
 aag ccg gtg caa gac cgg ggt ttg gtg gtg acg gac ctc aaa gct gag 254
 30 Lys Pro Val Gln Asp Arg Gly Leu Val Val Thr Asp Leu Lys Ala Glu
 45 50 55
 agt gtg gtt ctt gag cat cgc agc tac tgc tgc gca aag gcc cgg gac 302
 Ser Val Val Leu Glu His Arg Ser Tyr Cys Ser Ala Lys Ala Arg Asp
 60 65 70
 35 aga cac ttt gct ggg gat gta ctg ggc tat gtc act cca tgg aac agc 350

	Arg His Phe Ala Gly Asp Val Leu Gly Tyr Val Thr Pro Trp Asn Ser	
	75 80 85 90	
	cat ggc tac gat gtc acc aag gtc ttt ggg agc aag ttc aca cag atc	398
	His Gly Tyr Asp Val Thr Lys Val Phe Gly Ser Lys Phe Thr Gln Ile	
5	95 100 105	
	tca ccc gtc tgg ctg cag ctg aag aga cgt ggc cgt gag atg ttt gag	446
	Ser Pro Val Trp Leu Gln Leu Lys Arg Arg Gly Arg Glu Met Phe Glu	
	110 115 120	
	gtc acg ggc ctc cac gac gtg gac caa ggg tgg atg cga gct gtc agg	494
10	Val Thr Gly Leu His Asp Val Asp Gln Gly Trp Met Arg Ala Val Arg	
	125 130 135	
	aag cat gcc aag ggc ctg cac ata gtg cct cgg ctc ctg ttt gag gac	542
	Lys His Ala Lys Gly Leu His Ile Val Pro Arg Leu Leu Phe Glu Asp	
	140 145 150	
15	tgg act tac gat gat ttc cgg aac gtc tta gac agt gag gat gag ata	590
	Trp Thr Tyr Asp Asp Phe Arg Asn Val Leu Asp Ser Glu Asp Glu Ile	
	155 160 165 170	
	gag gag ctg agc aag acc gtg gtc cag gtg gca aag aac cag cat ttc	638
	Glu Glu Leu Ser Lys Thr Val Val Gln Val Ala Lys Asn Gln His Phe	
20	175 180 185	
	gat ggc ttc gtg gtg gag gtc tgg aac cag ctg cta agc cag aag cgc	686
	Asp Gly Phe Val Val Glu Val Trp Asn Gln Leu Leu Ser Gln Lys Arg	
	190 195 200	
	gtg ggc ctc atc cac atg ctc acc cac ttg gcc gag gct ctg cac cag	734
25	Val Gly Leu Ile His Met Leu Thr His Leu Ala Glu Ala Leu His Gln	
	205 210 215	
	gcc cgg ctg ctg gcc ctc ctg gtc atc ccg cct gcc atc acc ccc ggg	782
	Ala Arg Leu Leu Ala Leu Leu Val Ile Pro Pro Ala Ile Thr Pro Gly	
	220 225 230	
30	acc gac cag ctg ggc atg ttc acg cac aag gag ttt gag cag ctg gcc	830
	Thr Asp Gln Leu Gly Met Phe Thr His Lys Glu Phe Glu Gln Leu Ala	
	235 240 245 250	
	ccc gtg ctg gat ggt ttc agc ctc atg acc tac gac tac tct aca gcg	878
	Pro Val Leu Asp Gly Phe Ser Leu Met Thr Tyr Asp Tyr Ser Thr Ala	
35	255 260 265	

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	cat cag cct ggc cct aat gca ccc ctg tcc tgg gtt cga gcc tgc gtc	926
	His Gln Pro Gly Pro Asn Ala Pro Leu Ser Trp Val Arg Ala Cys Val	
	270 275 280	
5	cag gtc ctg gac ccg aag tcc aag tgg cga agc aaa atc ctc ctg ggg	974
	Gln Val Leu Asp Pro Lys Ser Lys Trp Arg Ser Lys Ile Leu Leu Gly	
	285 290 295	
	ctc aac ttc tat ggt atg gac tac gcg acc tcc aag gat gcc cgt gag	1022
	Leu Asn Phe Tyr Gly Met Asp Tyr Ala Thr Ser Lys Asp Ala Arg Glu	
	300 305 310	
10	cct gtt gtc ggg gcc agg tac atc cag aca ctg aag gac cac agg ccc	1070
	Pro Val Val Gly Ala Arg Tyr Ile Gln Thr Leu Lys Asp His Arg Pro	
	315 320 325 330	
	cgg atg gtg tgg gac agc cag gcc tca gag cac ttc ttc gag tac aag	1118
	Arg Met Val Trp Asp Ser Gln Ala Ser Glu His Phe Phe Glu Tyr Lys	
15	335 340 345	
	aag agc cgc agt ggg agg cac gtc gtc ttc tac cca acc ctg aag tcc	1166
	Lys Ser Arg Ser Gly Arg His Val Val Phe Tyr Pro Thr Leu Lys Ser	
	350 355 360	
20	ctg cag gtg cgg ctg gag ctg gcc cgg gag ctg ggc gtt ggg gtc tct	1214
	Leu Gln Val Arg Leu Glu Leu Ala Arg Glu Leu Gly Val Gly Val Ser	
	365 370 375	
	atc tgg gag ctg ggc cag ggc ctg gac tac ttc tac gac ctg ctc t	1260
	Ile Trp Glu Leu Gly Gln Gly Leu Asp Tyr Phe Tyr Asp Leu Leu	
	380 385 390	
25	aggtgggcat tgcggcctcc gcggtggacg tggtctttttc taagccatgg agtgagtgg	1320
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5	gag agc cct ggg atg cac cgg cca gag gcc atg ctg ctg ctg ctc acg	97
	Glu Ser Pro Gly Met His Arg Pro Glu Ala Met Leu Leu Leu Leu Thr	
	15 20 25 30	
	ctt gcc ctc ctg ggg ggc ccc acc tgg gca ggg aag atg tat ggc cct	145
	Leu Ala Leu Leu Gly Gly Pro Thr Trp Ala Gly Lys Met Tyr Gly Pro	
10	35 40 45	
	gga gga ggc aag tat ttc agc acc act gaa gac tac gac cat gaa atc	193
	Gly Gly Gly Lys Tyr Phe Ser Thr Thr Glu Asp Tyr Asp His Glu Ile	
	50 55 60	
	aca ggg ctg cgg gtg tct gta ggt ctt ctc ctg gtg aaa agt gtc cag	241
15	Thr Gly Leu Arg Val Ser Val Gly Leu Leu Leu Val Lys Ser Val Gln	
	65 70 75	
	gtg aaa ctt gga gac tcc tgg gac gtg aaa ctg gga gcc tta ggt ggg	289
	Val Lys Leu Gly Asp Ser Trp Asp Val Lys Leu Gly Ala Leu Gly Gly	
	80 85 90	
20	aat acc cag gaa gtc acc ctg cag cca ggc gaa tac atc aca aaa gtc	337
	Asn Thr Gln Glu Val Thr Leu Gln Pro Gly Glu Tyr Ile Thr Lys Val	
	95 100 105 110	
	ttt gtc gcc ttc caa gct ttc ctc cgg ggt atg gtc atg tac acc agc	385
	Phe Val Ala Phe Gln Ala Phe Leu Arg Gly Met Val Met Tyr Thr Ser	
25	115 120 125	
	aag gac cgc tat ttc tat ttt ggg aag ctt gat ggc cag atc tcc tct	433
	Lys Asp Arg Tyr Phe Tyr Phe Gly Lys Leu Asp Gly Gln Ile Ser Ser	
	130 135 140	
	gcc tac ccc agc caa gag ggg cag gtg ctg gtg ggc atc tat ggc cag	481
30	Ala Tyr Pro Ser Gln Glu Gly Gln Val Leu Val Gly Ile Tyr Gly Gln	
	145 150 155	
	tat caa ctc ctt ggc atc aag agc att ggc ttt gaa tgg aat tat cca	529
	Tyr Gln Leu Leu Gly Ile Lys Ser Ile Gly Phe Glu Trp Asn Tyr Pro	
	160 165 170	
35	cta gag gag ccg acc act gag cca cca gtt aat ctc aca tac tca gca	577

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Leu Glu Glu Pro Thr Thr Glu Pro Pro Val Asn Leu Thr Tyr Ser Ala
 175 180 185 190
 aac tca ccc gtg ggt cgc taggggtggg tatggggcca tccgagctga ggcca 630
 Asn Ser Pro Val Gly Arg
 5 195
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 accaataaat aaagcttctg c 711

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 20 atgagggagg agaggtggag ttgccggggc tcaggcccg cctcgagcat gggcggatga 180
 gaggagtcgg gagccgaggc ctagggtcct tcgggtgagg ggagacggag ccagcgagga 240
 g atg gag cag aag ctt gtg gag gag att ctt caa gca atc act atg 286
 Met Glu Gln Lys Leu Val Glu Glu Ile Leu Gln Ala Ile Thr Met
 1 5 10 15
 25 tca aca gac aca ggt gtt tcc ctt cct tca tat gag gaa gat cag gga 334
 Ser Thr Asp Thr Gly Val Ser Leu Pro Ser Tyr Glu Glu Asp Gln Gly
 20 25 30
 tca aaa ctc att cga aaa gct aaa gag gca cca ttc gta ccc gtt gga 382
 Ser Lys Leu Ile Arg Lys Ala Lys Glu Ala Pro Phe Val Pro Val Gly
 30 35 40 45
 ata gcg ggt ttt gca gca att gtt gca tat gga tta tat aaa ctg aag 430
 Ile Ala Gly Phe Ala Ala Ile Val Ala Tyr Gly Leu Tyr Lys Leu Lys
 50 55 60
 agc agg gga aat act aaa atg tcc att cat ctg atc cac atg cgt gtg 478
 35 Ser Arg Gly Asn Thr Lys Met Ser Ile His Leu Ile His Met Arg Val

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	65	70	75	
	gca gcc caa ggc ttt gtt gta gga gca atg act gtt ggt atg ggc tat			526
	Ala Ala Gln Gly Phe Val Val Gly Ala Met Thr Val Gly Met Gly Tyr			
	80	85	90	95
5	tcc atg tat cgg gaa ttc tgg gca aaa cct aag cct tagaagaa			570
	Ser Met Tyr Arg Glu Phe Trp Ala Lys Pro Lys Pro			
	100	105		
	gagatgctgt cttggtcttg ttggaggagc ttgctttagt tagatgtctt attattaaag			630
	ttacctatta ttgttgaaa t			651
10				
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	<211> 1310			
	<212> DNA			
	<213> Homo Sapience			
15	<220>			
	<221> CDS			
	<222> (78)...(1130)			
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20	cgaacgccaa ggcggccacg tectgetccc cctggtgaag aagetgccct gggettgtcg			60
	tectagggtc tccagac atg tct gag gtg aag agc cgg aag aag tcg ggg			110
	Met Ser Glu Val Lys Ser Arg Lys Lys Ser Gly			
	1	5	10	
	ccc aag gga gcc cct gct gcg gag ccc ggg aag cgg agc gag ggc ggg			158
25	Pro Lys Gly Ala Pro Ala Ala Glu Pro Gly Lys Arg Ser Glu Gly Gly			
	15	20	25	
	aag acc ccc gtg gcc cgg agc agc gga ggc ggg ggc tgg gca gac ccc			206
	Lys Thr Pro Val Ala Arg Ser Ser Gly Gly Gly Gly Trp Ala Asp Pro			
	30	35	40	
30	cga acg tgc ctg agc ctg ctg tcg ctg ggg acg tgc ctg ggc ctg gcc			254
	Arg Thr Cys Leu Ser Leu Leu Ser Leu Gly Thr Cys Leu Gly Leu Ala			
	45	50	55	
	tgg ttt gta ttt cag cag tca gaa aaa ttt gca aag gtg gaa aac caa			302
	Trp Phe Val Phe Gln Gln Ser Glu Lys Phe Ala Lys Val Glu Asn Gln			
35	60	65	70	75

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	tac cag tta ctg aaa cta gaa acc aat gaa ttc caa caa ctt caa agt	350
	Tyr Gln Leu Leu Lys Leu Glu Thr Asn Glu Phe Gln Gln Leu Gln Ser	
	80 85 90	
5	aaa atc agt tta att tca gaa aag tgg cag aaa tct gaa gct atc atg	398
	Lys Ile Ser Leu Ile Ser Glu Lys Trp Gln Lys Ser Glu Ala Ile Met	
	95 100 105	
	gaa caa ttg aag tct ttt caa ata att gct cat cta aag cgt cta cag	446
	Glu Gln Leu Lys Ser Phe Gln Ile Ile Ala His Leu Lys Arg Leu Gln	
	110 115 120	
10	gaa gaa att aat gag gta aaa act tgg tcc aat agg ata act gaa aaa	494
	Glu Glu Ile Asn Glu Val Lys Thr Trp Ser Asn Arg Ile Thr Glu Lys	
	125 130 135	
	cag gat ata ctg aac aac agt ctg acg acg ctt tct caa gac att aca	542
	Gln Asp Ile Leu Asn Asn Ser Leu Thr Thr Leu Ser Gln Asp Ile Thr	
15	140 145 150 155	
	aaa gta gac caa agt aca act tcc atg gca aaa gat gtt ggt ctc aag	590
	Lys Val Asp Gln Ser Thr Thr Ser Met Ala Lys Asp Val Gly Leu Lys	
	160 165 170	
20	att aca agt gta aaa aca gat ata cga cgg att tca ggt tta gta act	638
	Ile Thr Ser Val Lys Thr Asp Ile Arg Arg Ile Ser Gly Leu Val Thr	
	175 180 185	
	gat gta ata tca ttg aca gat tct gtg caa gaa cta gaa aat aaa ata	686
	Asp Val Ile Ser Leu Thr Asp Ser Val Gln Glu Leu Glu Asn Lys Ile	
	190 195 200	
25	gag aaa gta gaa aaa aat aca gta aaa aat ata ggt gat ctt ctt tca	734
	Glu Lys Val Glu Lys Asn Thr Val Lys Asn Ile Gly Asp Leu Leu Ser	
	205 210 215	
	agc agt att gat cga aca gca acg ctc cga aag aca gca tct gaa aat	782
	Ser Ser Ile Asp Arg Thr Ala Thr Leu Arg Lys Thr Ala Ser Glu Asn	
30	220 225 230 235	
	tca caa aga att aac tct gtt aag aag acg cta acc gaa cta aag agt	830
	Ser Gln Arg Ile Asn Ser Val Lys Lys Thr Leu Thr Glu Leu Lys Ser	
	240 245 250	
35	gac ttc gac aaa cat aca gat aga ttt cta agc tta gaa ggt gac aga	878
	Asp Phe Asp Lys His Thr Asp Arg Phe Leu Ser Leu Glu Gly Asp Arg	

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	255	260	265	
	gcc aaa gtt ctg aag aca gtg act ttt gca aat gat cta aaa cca aag	926		
	Ala Lys Val Leu Lys Thr Val Thr Phe Ala Asn Asp Leu Lys Pro Lys			
	270	275	280	
5	gtg tat aat cta aag aag gac ttt tcc cgt tta gaa cca tta gta aat	974		
	Val Tyr Asn Leu Lys Lys Asp Phe Ser Arg Leu Glu Pro Leu Val Asn			
	285	290	295	
	gat tta aca cta cgc att ggg aga ttg gtt acc gac tta cta caa aga	1022		
	Asp Leu Thr Leu Arg Ile Gly Arg Leu Val Thr Asp Leu Leu Gln Arg			
10	300	305	310	315
	gag aaa gaa att gct ttc tta agt gaa aaa ata tct aat tta aca ata	1070		
	Glu Lys Glu Ile Ala Phe Leu Ser Glu Lys Ile Ser Asn Leu Thr Ile			
	320	325	330	
	gtc caa gct gag att aag gat att aaa gat gaa ata gca cac att tca	1118		
15	Val Gln Ala Glu Ile Lys Asp Ile Lys Asp Glu Ile Ala His Ile Ser			
	335	340	345	
	gat atg aat tagtttgaca ttattgagat tagactaagg taattttttt aat	1170		
	Asp Met Asn			
	350			
20	gggacctctc atgagaagac tggtaaataca aaaataatga tattttggag caaaagtcac	1230		
	tttatattta atcctatttt gtacagtaaa aataaaaactt taaaacaggt tgattttcca	1290		
	aaataaatat gctaaaacct	1310		
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25	<211> 1400			
	<212> DNA			
	<213> Homo Sapience			
	<220>			
	<221> CDS			
30	<222> (233)...(556)			
	<400> 120			
	tggctgtatg ctattggagg gtggaaatca catctcctgt ttatccgtgt gcttgtagg	60		
	tgtcagccgc ccccccccc ccatatgcag atttactcgg catggtagtg gccagcttct	120		
35	aacacagctg gtatttcaag tctcctggga cctcactcag gaatgatacc cctcagtag	180		

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	aagcagcagg tgatcttaac tcctttcaaa gagcaggcct gtctgggaag cc atg	235
	Met	
	1	
5	tcc tca gca ggc aca gca acc cct ctg gaa atg gat cac aaa ctc act	283
	Ser Ser Ala Gly Thr Ala Thr Pro Leu Glu Met Asp His Lys Leu Thr	
	5 10 15	
	tct cag cca ggc agg cca agc ttc tat tgt aac agt agg cac agt ata	331
	Ser Gln Pro Gly Arg Pro Ser Phe Tyr Cys Asn Ser Arg His Ser Ile	
	20 25 30	
10	gtc gga tca tca cat cag ctg ggt ttt tgg ttt agt cat cta gag tcg	379
	Val Gly Ser Ser His Gln Leu Gly Phe Trp Phe Ser His Leu Glu Ser	
	35 40 45	
	tct gga cta aag gtc ttt cag gtc tcc ttg ccc tgt gag tgc gtg aac	427
	Ser Gly Leu Lys Val Phe Gln Val Ser Leu Pro Cys Glu Cys Val Asn	
15	50 55 60 65	
	ctc ccc acc cga att gcc tca gtt gtc ctg agc ctc atg tct ctc ctg	475
	Leu Pro Thr Arg Ile Ala Ser Val Val Leu Ser Leu Met Ser Leu Leu	
	70 75 80	
	gtg gtg ggc cag gcc cct gca tgg gaa ggg agc ctg ctg cgg ggc agg	523
20	Val Val Gly Gln Ala Pro Ala Trp Glu Gly Ser Leu Leu Arg Gly Arg	
	85 90 95	
	cca gct ggg ggt gct cac cta tgc gca gca tgaagttatt gaaggac	570
	Pro Ala Gly Gly Ala His Leu Cys Ala Ala	
	100 105	
25	tggttggtga tggttggtgag cgtatccttc atggccagcg cgaagtcggc caggtcagcc	630
	aggtgctgcc agegetctct ctggacttg tcttctgtg ccaggggacc gtggagaaag	690
	tgtcaggggc cgtcactgc agcagcctgc tctgctgcct tccctggcag tggtctgggg	750
	gtggattccc tacacctaga tggtcaaggc cttacttttc ctcccacaaa ggagtcgcag	810
	ccaagctagc tctgacttgc cactgtgaca aagttcacgt agcaggtcta ggcaaagact	870
30	gggcaattga gcagaggaga cggacctgtg agtctgacca cgaggcggac cccttcacct	930
	tggtctgggc tggtcctggt ccttaggttt tgtcaggttg tccttgtttg gatccctcaa	990
	ctaggtgata agcactggag ggggatgacc cgccttggaac gtgtttcttt aacctcatcc	1050
	atataatagg gccgtgggat ggttgtagag gtaaagcagg atgatggtgt tttaagacca	1110
	gagcttgga ccagggtcc tacacctaat tttctctcct ggtagctgaa caaaggtcta	1170
35	aattagctta acaaaagaac aggctgccgt cagccagagt tctgaaggcc atgctttcag	1230

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tttcccttgt tgacaattgc tctccagttc ctatgaaagc acagagcctt agggggcctg 1290
gccacagaac acaaccatct taggcctgag ctgtgaacag caggggggtg tgtgtctgtt 1350
ctgtttctct gcttgccgaa ctttctcaat aaacctatt tcttatttat 1400

5 <210> 121
<211> 483
<212> PRT
<213> Homo sapience

10 <400> 121
Met Lys Ala Phe His Thr Phe Cys Val Val Leu Leu Val Phe Gly Ser
1 5 10 15
Val Ser Glu Ala Lys Phe Asp Asp Phe Glu Asp Glu Glu Asp Ile Val
20 25 30
15 Glu Tyr Asp Asp Asn Asp Phe Ala Glu Phe Glu Asp Val Met Glu Asp
35 40 45
Ser Val Thr Glu Ser Pro Gln Arg Val Ile Ile Thr Glu Asp Asp Glu
50 55 60
Asp Glu Thr Thr Val Glu Leu Glu Gly Gln Asp Glu Asn Gln Glu Gly
20 65 70 75 80
Asp Phe Glu Asp Ala Asp Thr Gln Glu Gly Asp Thr Glu Ser Glu Pro
85 90 95
Tyr Asp Asp Glu Glu Phe Glu Gly Tyr Glu Asp Lys Pro Asp Thr Ser
100 105 110
25 Ser Ser Lys Asn Lys Asp Pro Ile Thr Ile Val Asp Val Pro Ala His
115 120 125
Leu Gln Asn Ser Trp Glu Ser Tyr Tyr Leu Glu Ile Leu Met Val Thr
130 135 140
Gly Leu Leu Ala Tyr Ile Met Asn Tyr Ile Ile Gly Lys Asn Lys Asn
30 145 150 155 160
Ser Arg Leu Ala Gln Ala Trp Phe Asn Thr His Arg Glu Leu Leu Glu
165 170 175
Ser Asn Phe Thr Leu Val Gly Asp Asp Gly Thr Asn Lys Glu Ala Thr
180 185 190
35 Ser Thr Gly Lys Leu Asn Gln Glu Asn Glu His Ile Tyr Asn Leu Trp

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	195	200	205
	Cys Ser Gly Arg Val Cys Cys Glu Gly Met Leu Ile Gln Leu Arg Phe		
	210	215	220
5	Leu Lys Arg Gln Asp Leu Leu Asn Val Leu Ala Arg Met Met Arg Pro		
	225	230	235 240
	Val Ser Asp Gln Val Gln Ile Lys Val Thr Met Asn Asp Glu Asp Met		
	245	250	255
	Asp Thr Tyr Val Phe Ala Val Gly Thr Arg Lys Ala Leu Val Arg Leu		
	260	265	270
10	Gln Lys Glu Met Gln Asp Leu Ser Glu Phe Cys Ser Asp Lys Pro Lys		
	275	280	285
	Ser Gly Ala Lys Tyr Gly Leu Pro Asp Ser Leu Ala Ile Leu Ser Glu		
	290	295	300
	Met Gly Glu Val Thr Asp Gly Met Met Asp Thr Lys Met Val His Phe		
15	305	310	315 320
	Leu Thr His Tyr Ala Asp Lys Ile Glu Ser Val His Phe Ser Asp Gln		
	325	330	335
	Phe Ser Gly Pro Lys Ile Met Gln Glu Glu Gly Gln Pro Leu Lys Leu		
	340	345	350
20	Pro Asp Thr Lys Arg Thr Leu Leu Phe Thr Phe Asn Val Pro Gly Ser		
	355	360	365
	Gly Asn Thr Tyr Pro Lys Asp Met Glu Ala Leu Leu Pro Leu Met Asn		
	370	375	380
	Met Val Ile Tyr Ser Ile Asp Lys Ala Lys Lys Phe Arg Leu Asn Arg		
25	385	390	395 400
	Glu Gly Lys Gln Lys Ala Asp Lys Asn Arg Ala Arg Val Glu Glu Asn		
	405	410	415
	Phe Leu Lys Leu Thr His Val Gln Arg Gln Glu Ala Ala Gln Ser Arg		
	420	425	430
30	Arg Glu Glu Lys Lys Arg Ala Glu Lys Glu Arg Ile Met Asn Glu Glu		
	435	440	445
	Asp Pro Glu Lys Gln Arg Arg Leu Glu Glu Ala Ala Leu Arg Arg Glu		
	450	455	460
	Gln Lys Lys Leu Glu Lys Lys Gln Met Lys Met Lys Gln Ile Lys Val		
35	465	470	475 480

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Lys Ala Met

<210> 122

<211> 334

5 <212> PRT

<213> Homo sapience

<400> 122

10 Met Val Glu Phe Ala Pro Leu Phe Met Pro Trp Glu Arg Arg Leu Gln
 1 5 10 15
 Thr Leu Ala Val Leu Gln Phe Val Phe Ser Phe Leu Ala Leu Ala Glu
 20 25 30
 Ile Cys Thr Val Gly Phe Ile Ala Leu Leu Phe Thr Arg Phe Trp Leu
 35 40 45
 15 Leu Thr Val Leu Tyr Ala Ala Trp Trp Tyr Leu Asp Arg Asp Lys Pro
 50 55 60
 Arg Gln Gly Gly Arg His Ile Gln Ala Ile Arg Cys Trp Thr Ile Trp
 65 70 75 80
 Lys Tyr Met Lys Asp Tyr Phe Pro Ile Ser Leu Val Lys Thr Ala Glu
 20 85 90 95
 Leu Asp Pro Ser Arg Asn Tyr Ile Ala Gly Phe His Pro His Gly Val
 100 105 110
 Leu Ala Val Gly Ala Phe Ala Asn Leu Cys Thr Glu Ser Thr Gly Phe
 115 120 125
 25 Ser Ser Ile Phe Pro Gly Ile Arg Pro His Leu Met Met Leu Thr Leu
 130 135 140
 Trp Phe Arg Ala Pro Phe Phe Arg Asp Tyr Ile Met Ser Ala Gly Leu
 145 150 155 160
 Val Thr Ser Glu Lys Glu Ser Ala Ala His Ile Leu Asn Arg Lys Gly
 30 165 170 175
 Gly Gly Asn Leu Leu Gly Ile Ile Val Gly Gly Ala Gln Glu Ala Leu
 180 185 190
 Asp Ala Arg Pro Gly Ser Phe Thr Leu Leu Leu Arg Asn Arg Lys Gly
 195 200 205
 35 Phe Val Arg Leu Ala Leu Thr His Gly Ala Pro Leu Val Pro Ile Phe

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210 215 220
 Ser Phe Gly Glu Asn Asp Leu Phe Asp Gln Ile Pro Asn Ser Ser Gly
 225 230 235 240
 Ser Trp Leu Arg Tyr Ile Gln Asn Arg Leu Gln Lys Ile Met Gly Ile
 5 245 250 255
 Ser Leu Pro Leu Phe His Gly Arg Gly Val Phe Gln Tyr Ser Phe Gly
 260 265 270
 Leu Ile Pro Tyr Arg Arg Pro Ile Thr Thr Val Val Gly Lys Pro Ile
 275 280 285
 10 Glu Val Gln Lys Thr Leu His Pro Ser Glu Glu Glu Val Asn Gln Leu
 290 295 300
 His Gln Arg Tyr Ile Lys Glu Leu Cys Asn Leu Phe Glu Ala His Lys
 305 310 315 320
 Leu Lys Phe Asn Ile Pro Ala Asp Gln His Leu Glu Phe Cys
 15 325 330

 <210> 123
 <211> 267
 <212> PRT
 20 <213> Homo sapience .

 <400> 123
 Met Ala Pro Trp Ala Leu Leu Ser Pro Gly Val Leu Val Arg Thr Gly
 1 5 10 15
 25 His Thr Val Leu Thr Trp Gly Ile Thr Leu Val Leu Phe Leu His Asp
 20 25 30
 Thr Glu Leu Arg Gln Trp Glu Glu Gln Gly Glu Leu Leu Leu Pro Leu
 35 40 45
 Thr Phe Leu Leu Leu Val Leu Gly Ser Leu Leu Leu Tyr Leu Ala Val
 30 50 55 60
 Ser Leu Met Asp Pro Gly Tyr Val Asn Val Gln Pro Gln Pro Gln Glu
 65 70 75 80
 Glu Leu Lys Glu Glu Gln Thr Ala Met Val Pro Pro Ala Ile Pro Leu
 85 90 95
 35 Arg Arg Cys Arg Tyr Cys Leu Val Leu Gln Pro Leu Arg Ala Arg His

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100 105 110
 Cys Arg Glu Cys Arg Arg Cys Val Arg Arg Tyr Asp His His Cys Pro
 115 120 125
 Trp Met Glu Asn Cys Val Gly Glu Arg Asn His Pro Leu Phe Val Val
 5 130 135 140
 Tyr Leu Ala Leu Gln Leu Val Val Leu Leu Trp Gly Leu Tyr Leu Ala
 145 150 155 160
 Trp Ser Gly Leu Arg Phe Phe Gln Pro Trp Gly Leu Trp Leu Arg Ser
 165 170 175
 10 Ser Gly Leu Leu Phe Ala Thr Phe Leu Leu Leu Ser Leu Phe Ser Leu
 180 185 190
 Val Ala Ser Leu Leu Leu Val Ser His Leu Tyr Leu Val Ala Ser Asn
 195 200 205
 Thr Thr Thr Trp Glu Phe Ile Ser Ser His Arg Ile Ala Tyr Leu Arg
 15 210 215 220
 Gln Arg Pro Ser Asn Pro Phe Asp Arg Gly Leu Thr Arg Asn Leu Ala
 225 230 235 240
 His Phe Phe Cys Gly Trp Pro Ser Gly Ser Trp Glu Thr Leu Trp Ala
 245 250 255
 20 Glu Glu Glu Glu Glu Gly Ser Ser Pro Ala Val
 260 265

 <210> 124
 <211> 106
 25 <212> PRT
 <213> Homo sapience

 <400> 124
 Met Ser Thr Asn Asn Met Ser Asp Pro Arg Arg Pro Asn Lys Val Leu
 30 1 5 10 15
 Arg Tyr Lys Pro Pro Pro Ser Glu Cys Asn Pro Ala Leu Asp Asp Pro
 20 25 30
 Thr Pro Asp Tyr Met Asn Leu Leu Gly Met Ile Phe Ser Met Cys Gly
 35 40 45
 35 Leu Met Leu Lys Leu Lys Trp Cys Ala Trp Val Ala Val Tyr Cys Ser

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50 55 60
 Phe Ile Ser Phe Ala Asn Ser Arg Ser Ser Glu Asp Thr Lys Gln Met
 65 70 75 80
 Met Ser Ser Phe Met Leu Ser Ile Ser Ala Val Val Met Ser Tyr Leu
 5 85 90 95
 Gln Asn Pro Gln Pro Met Thr Pro Pro Trp
 100 105

 <210> 125
 10 <211> 224
 <212> PRT
 <213> Homo sapience

 <400> 125
 15 Met Thr Leu Phe His Phe Gly Asn Cys Phe Ala Leu Ala Tyr Phe Pro
 1 5 10 15
 Tyr Phe Ile Thr Tyr Lys Cys Ser Gly Leu Ser Glu Tyr Asn Ala Phe
 20 20 25 30
 Trp Lys Cys Val Gln Ala Gly Val Thr Tyr Leu Phe Val Gln Leu Cys
 20 35 40 45
 Lys Met Leu Phe Leu Ala Thr Phe Phe Pro Thr Trp Glu Gly Gly Ile
 50 55 60
 Tyr Asp Phe Ile Gly Glu Phe Met Lys Ala Ser Val Asp Val Ala Asp
 65 70 75 80
 25 Leu Ile Gly Leu Asn Leu Val Met Ser Arg Asn Ala Gly Lys Gly Glu
 85 90 95
 Tyr Lys Ile Met Val Ala Ala Leu Gly Trp Ala Thr Ala Glu Leu Ile
 100 105 110
 Met Ser Arg Cys Ile Pro Leu Trp Val Gly Ala Arg Gly Ile Glu Phe
 30 115 120 125
 Asp Trp Lys Tyr Ile Gln Met Ser Ile Asp Ser Asn Ile Ser Leu Val
 130 135 140
 His Tyr Ile Val Ala Ser Ala Gln Val Trp Met Ile Thr Arg Tyr Asp
 145 150 155 160
 35 Leu Tyr His Thr Phe Arg Pro Ala Val Leu Leu Leu Met Phe Leu Ser

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165 170 175
 Val Tyr Lys Ala Phe Val Met Glu Thr Phe Val His Leu Cys Ser Leu
 180 185 190
 Gly Ser Trp Ala Ala Leu Leu Ala Arg Ala Val Val Thr Gly Leu Leu
 5 195 200 205
 Ala Leu Ser Thr Leu Ala Leu Tyr Val Ala Val Val Asn Val His Ser
 210 215 220

 <210> 126
 10 <211> 258
 <212> PRT
 <213> Homo sapience

 <400> 126
 15 Met Ala Val Leu Ala Pro Leu Ile Ala Leu Val Tyr Ser Val Pro Arg
 1 5 10 15
 Leu Ser Arg Trp Leu Ala Gln Pro Tyr Tyr Leu Leu Ser Ala Leu Leu
 20 25 30
 Ser Ala Ala Phe Leu Leu Val Arg Lys Leu Pro Pro Leu Cys His Gly
 20 35 40 45
 Leu Pro Thr Gln Arg Glu Asp Gly Asn Pro Cys Asp Phe Asp Trp Arg
 50 55 60
 Glu Val Glu Ile Leu Met Phe Leu Ser Ala Ile Val Met Met Lys Asn
 65 70 75 80
 25 Arg Arg Ser Met Phe Leu Met Thr Cys Lys Pro Pro Leu Tyr Met Gly
 85 90 95
 Pro Glu Tyr Ile Lys Tyr Phe Asn Asp Lys Thr Ile Asp Glu Glu Leu
 100 105 110
 Glu Arg Asp Lys Arg Val Thr Trp Ile Val Glu Phe Phe Ala Asn Trp
 115 120 125
 Ser Asn Asp Cys Gln Ser Phe Ala Pro Ile Tyr Ala Asp Leu Ser Leu
 130 135 140
 Lys Tyr Asn Cys Thr Gly Leu Asn Phe Gly Lys Val Asp Val Gly Arg
 145 150 155 160
 35 Tyr Thr Asp Val Ser Thr Arg Tyr Lys Val Ser Thr Ser Pro Leu Thr

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165 170 175
 Lys Gln Leu Pro Thr Leu Ile Leu Phe Gln Gly Gly Lys Glu Ala Met
 180 185 190
 Arg Arg Pro Gln Ile Asp Lys Lys Gly Arg Ala Val Ser Trp Thr Phe
 5 195 200 205
 Ser Glu Glu Asn Val Ile Arg Glu Phe Asn Leu Asn Glu Leu Tyr Gln
 210 215 220
 Arg Ala Lys Lys Leu Ser Lys Ala Gly Asp Asn Ile Pro Glu Glu Gln
 225 230 235 240
 10 Pro Val Ala Ser Thr Pro Thr Thr Val Ser Asp Gly Glu Asn Lys Lys
 245 250 255
 Asp Lys

 <210> 127
 15 <211> 110
 <212> PRT
 <213> Homo sapience

 <400> 127
 20 Met Ala Ala Val Val Ala Lys Arg Glu Gly Pro Pro Phe Ile Ser Glu
 1 5 10 15
 Ala Ala Val Arg Gly Asn Ala Ala Val Leu Asp Tyr Cys Arg Thr Ser
 20 25 30
 Val Ser Ala Leu Ser Gly Ala Thr Ala Gly Ile Leu Gly Leu Thr Gly
 25 35 40 45
 Leu Tyr Gly Phe Ile Phe Tyr Leu Leu Ala Ser Val Leu Leu Ser Leu
 50 55 60
 Leu Leu Ile Leu Lys Ala Gly Arg Arg Trp Asn Lys Tyr Phe Lys Ser
 65 70 75 80
 30 Arg Arg Pro Leu Phe Thr Gly Gly Leu Ile Gly Gly Leu Phe Thr Tyr
 85 90 95
 Val Leu Phe Trp Thr Phe Leu Tyr Gly Met Val His Val Tyr
 100 105 110

 35 <210> 128

147/177

<211> 91

<212> PRT

<213> Homo sapience

5 <400> 128

Met Val Tyr Ile Ser Asn Gly Gln Val Leu Asp Ser Arg Ser Gln Ser

1 5 10 15

Pro Trp Arg Leu Ser Leu Ile Thr Asp Phe Phe Trp Gly Ile Ala Glu

20 25 30

10 Phe Val Val Leu Phe Phe Lys Thr Leu Leu Gln Gln Asp Val Lys Lys

35 40 45

Arg Arg Ser Tyr Gly Asn Ser Ser Asp Ser Arg Tyr Asp Asp Gly Arg

50 55 60

Gly Pro Pro Gly Asn Pro Pro Arg Arg Met Gly Arg Ile Asn His Leu

15 65 70 75 80

Arg Gly Pro Ser Pro Pro Pro Met Ala Gly Gly

85 90

<210> 129

20 <211> 344

<212> PRT

<213> Homo sapience

<400> 129

25 Met Phe Thr Ser Thr Gly Ser Ser Gly Leu Tyr Lys Ala Pro Leu Ser

1 5 10 15

Lys Ser Leu Leu Leu Val Pro Ser Ala Leu Ser Leu Leu Leu Ala Leu

20 25 30

Leu Leu Pro His Cys Gln Lys Leu Phe Val Tyr Asp Leu His Ala Val

30 35 40 45

Lys Asn Asp Phe Gln Ile Trp Arg Leu Ile Cys Gly Arg Ile Ile Cys

50 55 60

Leu Asp Leu Lys Asp Thr Phe Cys Ser Ser Leu Leu Ile Tyr Asn Phe

65 70 75 80

35 Arg Ile Phe Glu Arg Arg Tyr Gly Ser Arg Lys Phe Ala Ser Phe Leu

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	85	90	95
	Leu Gly Ser Trp Val Leu Ser Ala Leu Phe Asp Phe Leu Leu Ile Glu		
	100	105	110
	Ala Met Gln Tyr Phe Phe Gly Ile Thr Ala Ala Ser Asn Leu Pro Ser		
5	115	120	125
	Gly Phe Leu Ala Pro Val Phe Ala Leu Phe Val Pro Phe Tyr Cys Ser		
	130	135	140
	Ile Pro Arg Val Gln Val Ala Gln Ile Leu Gly Pro Leu Ser Ile Thr		
	145	150	155
10	Asn Lys Thr Leu Ile Tyr Ile Leu Gly Leu Gln Leu Phe Thr Ser Gly		
	165	170	175
	Ser Tyr Ile Trp Ile Val Ala Ile Ser Gly Leu Met Ser Gly Leu Cys		
	180	185	190
	Tyr Asp Ser Lys Met Phe Gln Val His Gln Val Leu Cys Ile Pro Ser		
15	195	200	205
	Trp Met Ala Lys Phe Phe Ser Trp Thr Leu Glu Pro Ile Phe Ser Ser		
	210	215	220
	Ser Glu Pro Thr Ser Glu Ala Arg Ile Gly Met Gly Ala Thr Leu Asp		
	225	230	235
20	Ile Gln Arg Gln Gln Arg Met Glu Leu Leu Asp Arg Gln Leu Met Phe		
	245	250	255
	Ser Gln Phe Ala Gln Gly Arg Arg Gln Arg Gln Gln Gln Gly Gly Met		
	260	265	270
	Ile Asn Trp Asn Arg Leu Phe Pro Pro Leu Arg Gln Arg Gln Asn Val		
25	275	280	285
	Asn Tyr Gln Gly Gly Arg Gln Ser Glu Pro Ala Ala Pro Pro Leu Glu		
	290	295	300
	Val Ser Glu Glu Gln Val Ala Arg Leu Met Glu Met Gly Phe Ser Arg		
	305	310	315
30	Gly Asp Ala Leu Glu Ala Leu Arg Ala Ser Asn Asn Asp Leu Asn Val		
	325	330	335
	Ala Thr Asn Phe Leu Leu Gln His		
	340		
35	<210> 130		

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<211> 428

<212> PRT

<213> Homo sapience

5 <400> 130

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Met Gly Pro Pro Pro Gly Ala Gly Val Ser Cys Arg Gly Gly Cys Gly
  1             5             10             15
Phe Ser Arg Leu Leu Ala Trp Cys Phe Leu Leu Ala Leu Ser Pro Gln
          20             25             30
10 Ala Pro Gly Ser Arg Gly Ala Glu Ala Val Trp Thr Ala Tyr Leu Asn
      35             40             45
Val Ser Trp Arg Val Pro His Thr Gly Val Asn Arg Thr Val Trp Glu
      50             55             60
Leu Ser Glu Glu Gly Val Tyr Gly Gln Asp Ser Pro Leu Glu Pro Val
15  65             70             75             80
Ala Gly Val Leu Val Pro Pro Asp Gly Pro Gly Ala Leu Asn Ala Cys
          85             90             95
Asn Pro His Thr Asn Phe Thr Val Pro Thr Val Trp Gly Ser Thr Val
          100            105            110
20 Gln Val Ser Trp Leu Ala Leu Ile Gln Arg Gly Gly Gly Cys Thr Phe
      115            120            125
Ala Asp Lys Ile His Leu Ala Tyr Glu Arg Gly Ala Ser Gly Ala Val
      130            135            140
Ile Phe Asn Phe Pro Gly Thr Arg Asn Glu Val Ile Pro Met Ser His
25  145            150            155            160
Pro Gly Ala Val Asp Ile Val Ala Ile Met Ile Gly Asn Leu Lys Gly
          165            170            175
Thr Lys Ile Leu Gln Ser Ile Gln Arg Gly Ile Gln Val Thr Met Val
          180            185            190
30 Ile Glu Val Gly Lys Lys His Gly Pro Trp Val Asn His Tyr Ser Ile
      195            200            205
Phe Phe Val Ser Val Ser Phe Phe Ile Ile Thr Ala Ala Thr Val Gly
          210            215            220
Tyr Phe Ile Phe Tyr Ser Ala Arg Arg Leu Arg Asn Ala Arg Ala Gln
35  225            230            235            240

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	Arg Leu Gln Leu Arg Thr Leu Lys Gln Gly Asp Lys Glu Ile Gly Pro	
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5	Asp Gly Asp Ser Cys Ala Val Cys Ile Glu Leu Tyr Lys Pro Asn Asp	
	275	280 285
	Leu Val Arg Ile Leu Thr Cys Asn His Ile Phe His Lys Thr Cys Val	
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	Asp Pro Trp Leu Leu Glu His Arg Thr Cys Pro Met Cys Lys Cys Asp	
10	305	310 315 320
	Ile Leu Lys Ala Leu Gly Ile Glu Val Asp Val Glu Asp Gly Ser Val	
	325	330 335
	Ser Leu Gln Val Pro Val Ser Asn Glu Ile Ser Asn Ser Ala Ser Ser	
	340	345 350
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	Val Gln Gly Thr Asp Glu Pro Pro Leu Glu Glu His Val Gln Ser Thr	
	370	375 380
	Asn Glu Ser Leu Gln Leu Val Asn His Glu Ala Asn Ser Val Ala Val	
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	Pro Asn Gln Glu Thr Ala Val Arg Glu Ile Lys Ser	
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	aatgagcaca tctataacct gtggtgttct ggtcgagtgt gctgtgaggg catgcttatc	660
	cagctgaggt tcctcaagag acaagactta ctgaatgtcc tggcccggat gatgaggcca	720
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	cggaaactaca ttgcgggctt ccacccccat ggagtcttg cagtcggagc ctttgccaac	360
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15 <213> Homo sapience

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 20 cagggggagc tgetcctgcc cctcaccttc ctgetcctgg tgctgggctc cctgctgctc 180
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 gcctatctcc gccagcgccc cagcaacccc ttccagcgag gcctgacctg caacctggcc 720
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<210> 134

<211> 318

35 <212> DNA

153/177

<213> Homo sapience

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 ggcattgatc tcagcatgtg cggcctcatg ctttaagctga agtgggtgtg ttgggtgctg 180
 gtctactgct ccttcacag ctttgccaac tctcggagct cggaggacac gaagcaaagt 240
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10

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<211> 672

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15

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 acctacctt ttgtccaact ctgcaagatg ctgttcttg ccactttctt tcccacctgg 180
 gaaggcggca tctatgactt cattggggag ttcattgaagg ccagcgtgga tgtggcagac 240
 ctgataggtc taaaccttgt catgtcccg aatgccggca agggagagta caagatcatg 300
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 tttgttatgg agaccttcgt ccacctctgc tcgctgggca gttgggcagc tctactggcc 600
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30

<210> 136

<211> 774

<212> DNA

<213> Homo sapience

35

<400> 136

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	aagtacttca atgataaaac cattgatgag gaactagaac gggacaagag ggtcacttgg	360
	attgtggagt tctttgccaa ttggtctaat gactgccaat catttgcccc tatctatget	420
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	gagctatacc agcggggccaa gaaactatca aaggtctggag acaatatccc tgaggagcag	720
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	gccggcatcc tcggcctcac cggcctctac ggettcattc tctacctget cgcctccgtc	180
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	gcagtgtgga ccgcgtacct caacgtgtcc tggcgggttc cgcacacggg agtgaaccgt	180
	acggtgtggg agctgagcga ggagggcggtg tacggccagg actcgccgct ggagcctgtg	240
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	aatttcacgg tgcccacggt ttggggaagc accgtgcaag tctcttggtt ggccctcatc	360
	caacgcggcg ggggctgcac cttegcagac aagatccatc tggcttatga gagaggggcg	420
	tctggagccg tcatctttaa ctccccggg acccgcaatg aggtcatecc catgtctcac	480
	ccgggtgcag tagacattgt tgcaatcatg atcggcaatc tgaaaggcac aaaaattctg	540
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	gcaactgtgg gctattttat cttttattct gctcgaagc tacggaatgc aagagctcaa	720
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Met Lys Ala Phe His Thr Phe Cys Val Val Leu Leu Val Phe Gly

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Ser Val Ser Glu Ala Lys Phe Asp Asp Phe Glu Asp Glu Glu Asp Ile

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gta gag tat gat gat aat gac ttc gct gaa ttt gag gat gtc atg gaa 262

Val Glu Tyr Asp Asp Asn Asp Phe Ala Glu Phe Glu Asp Val Met Glu

35 40 45

gac tct gtt act gaa tct cct caa cgg gtc ata atc act gaa gat gat 310

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50 55 60

gaa gat gag acc act gtg gag ttg gaa ggg cag gat gaa aac caa gaa 358

Glu Asp Glu Thr Thr Val Glu Leu Glu Gly Gln Asp Glu Asn Gln Glu

65 70 75

15 gga gat ttt gaa gat gca gat acc cag gag gga gat act gag agt gaa 406

Gly Asp Phe Glu Asp Ala Asp Thr Gln Glu Gly Asp Thr Glu Ser Glu

80 85 90 95

cca tat gat gat gaa gaa ttt gaa ggt tat gaa gac aaa cca gat act 454

Pro Tyr Asp Asp Glu Glu Phe Glu Gly Tyr Glu Asp Lys Pro Asp Thr

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tct tct agc aaa aat aaa gac cca ata acg att gtt gat gtt cct gca 502

Ser Ser Ser Lys Asn Lys Asp Pro Ile Thr Ile Val Asp Val Pro Ala

115 120 125

cac ctc cag aac agc tgg gag agt tat tat cta gaa att ttg atg gtg 550

25 His Leu Gln Asn Ser Trp Glu Ser Tyr Tyr Leu Glu Ile Leu Met Val

130 135 140

act ggt ctg ctt gct tat atc atg aat tac atc att ggg aag aat aaa 598

Thr Gly Leu Leu Ala Tyr Ile Met Asn Tyr Ile Ile Gly Lys Asn Lys

145 150 155

30 aac agt cgc ctt gca cag gcc tgg ttt aac act cat agg gag ctt ttg 646

Asn Ser Arg Leu Ala Gln Ala Trp Phe Asn Thr His Arg Glu Leu Leu

160 165 170 175

gag agc aac ttt act tta gtg ggg gat gat gga act aac aaa gaa gcc 694

Glu Ser Asn Phe Thr Leu Val Gly Asp Asp Gly Thr Asn Lys Glu Ala

35 180 185 190

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5	Trp Cys Ser Gly Arg Val Cys Cys Glu Gly Met Leu Ile Gln Leu Arg	
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	ttc ctc aag aga caa gac tta ctg aat gtc ctg gcc cgg atg atg agg	838
	Phe Leu Lys Arg Gln Asp Leu Leu Asn Val Leu Ala Arg Met Met Arg	
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	Pro Val Ser Asp Gln Val Gln Ile Lys Val Thr Met Asn Asp Glu Asp	
	240 245 250 255	
	atg gat acc tac gta ttt gct gtt ggc aca cgg aaa gcc ttg gtg cga	934
	Met Asp Thr Tyr Val Phe Ala Val Gly Thr Arg Lys Ala Leu Val Arg	
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	cta cag aaa gag atg cag gat ttg agt gag ttt tgt agt gat aaa cct	982
	Leu Gln Lys Glu Met Gln Asp Leu Ser Glu Phe Cys Ser Asp Lys Pro	
	275 280 285	
	aag tct gga gca aag tat gga ctg ccg gac tct ttg gcc atc ctg tca	1030
20	Lys Ser Gly Ala Lys Tyr Gly Leu Pro Asp Ser Leu Ala Ile Leu Ser	
	290 295 300	
	gag atg gga gaa gtc aca gac gga atg atg gat aca aag atg gtt cac	1078
	Glu Met Gly Glu Val Thr Asp Gly Met Met Asp Thr Lys Met Val His	
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25	ttt ctt aca cac tat gct gac aag att gaa tct gtt cat ttt tca gac	1126
	Phe Leu Thr His Tyr Ala Asp Lys Ile Glu Ser Val His Phe Ser Asp	
	320 325 330 335	
	cag ttc tct ggt cca aaa att atg caa gag gaa ggt cag cct tta aag	1174
	Gln Phe Ser Gly Pro Lys Ile Met Gln Glu Glu Gly Gln Pro Leu Lys	
30	340 345 350	
	cta cct gac act aag agg aca ctg ttg ttt aca ttt aat gtg cct ggc	1222
	Leu Pro Asp Thr Lys Arg Thr Leu Leu Phe Thr Phe Asn Val Pro Gly	
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	tca ggt aac act tac cca aag gat atg gag gca ctg cta ccc ctg atg	1270
35	Ser Gly Asn Thr Tyr Pro Lys Asp Met Glu Ala Leu Leu Pro Leu Met	

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	370	375	380	
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	Asn Met Val Ile Tyr Ser Ile Asp Lys Ala Lys Lys Phe Arg Leu Asn			
	385	390	395	
5	aga gaa ggc aaa caa aaa gca gat aag aac cgt gcc cga gta gaa gag			1366
	Arg Glu Gly Lys Gln Lys Ala Asp Lys Asn Arg Ala Arg Val Glu Glu			
	400	405	410	415
	aac ttc ttg aaa ctg aca cat gtg caa aga cag gaa gca gca cag tct			1414
	Asn Phe Leu Lys Leu Thr His Val Gln Arg Gln Glu Ala Ala Gln Ser			
10	420	425	430	
	cgg cgg gag gag aaa aaa aga gca gag aag gag cga atc atg aat gag			1462
	Arg Arg Glu Glu Lys Lys Arg Ala Glu Lys Glu Arg Ile Met Asn Glu			
	435	440	445	
	gaa gat cct gag aaa cag cgc agg ctg gag gag gct gca ttg agg cgt			1510
15	Glu Asp Pro Glu Lys Gln Arg Arg Leu Glu Glu Ala Ala Leu Arg Arg			
	450	455	460	
	gag caa aag aag ttg gaa aag aag caa atg aaa atg aaa caa atc aaa			1558
	Glu Gln Lys Lys Leu Glu Lys Lys Gln Met Lys Met Lys Gln Ile Lys			
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20	gtg aaa gcc atg taaagccatc ccagagattt gagttctgat gccacctgta			1610
	Val Lys Ala Met			
	480			
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	taccatgaaa tttataggta gataaccaga ttgttgcttt ttgtttaaac caagcagttg			1970
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	<211> 2746			
	<212> DNA			
35	<213> Homo sapience			

160/177

<220>

<221> CDS

<222> (70)...(1074)

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Met Val Glu Phe Ala Pro Leu Phe Met Pro Trp Glu Arg

1 5 10

10 agg ctg cag aca ctt gct gtc cta cag ttt gtc ttc tcc ttc ttg gca 156

Arg Leu Gln Thr Leu Ala Val Leu Gln Phe Val Phe Ser Phe Leu Ala

15 20 25

ctg gcc gag atc tgc act gtg ggc ttc ata gcc ctc ctg ttt aca aga 204

Leu Ala Glu Ile Cys Thr Val Gly Phe Ile Ala Leu Leu Phe Thr Arg

15 30 35 40 45

ttc tgg ctc ctc act gtc ctg tat gcg gcc tgg tgg tat ctg gac cga 252

Phe Trp Leu Leu Thr Val Leu Tyr Ala Ala Trp Trp Tyr Leu Asp Arg

50 55 60

gac aag cca cgg cag ggg ggc cgg cac atc cag gcc atc agg tgc tgg 300

20 Asp Lys Pro Arg Gln Gly Gly Arg His Ile Gln Ala Ile Arg Cys Trp

65 70 75

act ata tgg aag tac atg aag gac tat ttc ccc atc tcg ctg gtc aag 348

Thr Ile Trp Lys Tyr Met Lys Asp Tyr Phe Pro Ile Ser Leu Val Lys

80 85 90

25 act gct gag ctg gac ccc tct cgg aac tac att gcg ggc ttc cac ccc 396

Thr Ala Glu Leu Asp Pro Ser Arg Asn Tyr Ile Ala Gly Phe His Pro

95 100 105

cat gga gtc ctg gca gtc gga gcc ttt gcc aac ctg tgc act gag agc 444

His Gly Val Leu Ala Val Gly Ala Phe Ala Asn Leu Cys Thr Glu Ser

30 110 115 120 125

aca ggc ttc tct tcg atc ttc ccc ggt atc cgc ccc cat ctg atg atg 492

Thr Gly Phe Ser Ser Ile Phe Pro Gly Ile Arg Pro His Leu Met Met

130 135 140

ctg acc ttg tgg ttc cgg gcc ccc ttc ttc aga gat tac atc atg tct 540

35 Leu Thr Leu Trp Phe Arg Ala Pro Phe Phe Arg Asp Tyr Ile Met Ser

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	145	150	155	
	gca ggg ttg gtc aca tca gaa aag gag agt gct gct cac att ctg aac	588		
	Ala Gly Leu Val Thr Ser Glu Lys Glu Ser Ala Ala His Ile Leu Asn			
	160	165	170	
5	agg aag ggt ggc gga aac ttg ctg ggc atc att gta ggg ggt gcc cag	636		
	Arg Lys Gly Gly Gly Asn Leu Leu Gly Ile Ile Val Gly Gly Ala Gln			
	175	180	185	
	gag gcc ctg gat gcc agg cct gga tcc ttc acg ctg tta ctg cgg aac	684		
	Glu Ala Leu Asp Ala Arg Pro Gly Ser Phe Thr Leu Leu Leu Arg Asn			
10	190	195	200	205
	cga aag ggc ttc gtc agg ctc gcc ctg aca cac ggg gca ccc ctg gtg	732		
	Arg Lys Gly Phe Val Arg Leu Ala Leu Thr His Gly Ala Pro Leu Val			
	210	215	220	
	cca atc ttc tcc ttc ggg gag aat gac cta ttt gac cag att ccc aac	780		
15	Pro Ile Phe Ser Phe Gly Glu Asn Asp Leu Phe Asp Gln Ile Pro Asn			
	225	230	235	
	tct tct ggc tcc tgg tta cgc tat atc cag aat cgg ttg cag aag atc	828		
	Ser Ser Gly Ser Trp Leu Arg Tyr Ile Gln Asn Arg Leu Gln Lys Ile			
	240	245	250	
20	atg ggc atc tcc ctc cca ctc ttt cat ggc cgt ggt gtc ttc cag tac	876		
	Met Gly Ile Ser Leu Pro Leu Phe His Gly Arg Gly Val Phe Gln Tyr			
	255	260	265	
	agc ttt ggt tta ata ccc tac cgc cgg ccc atc acc act gtg gtg ggg	924		
	Ser Phe Gly Leu Ile Pro Tyr Arg Arg Pro Ile Thr Thr Val Val Gly			
25	270	275	280	285
	aag ccc atc gag gta cag aag acg ctg cat ccc tcg gag gag gag gtg	972		
	Lys Pro Ile Glu Val Gln Lys Thr Leu His Pro Ser Glu Glu Glu Val			
	290	295	300	
	aac cag ctg cac cag cgt tat atc aaa gag ctg tgc aac ctc ttc gag	1020		
30	Asn Gln Leu His Gln Arg Tyr Ile Lys Glu Leu Cys Asn Leu Phe Glu			
	305	310	315	
	gcc cac aaa ctt aag ttc aac atc cct gct gac cag cac ttg gag ttc	1068		
	Ala His Lys Leu Lys Phe Asn Ile Pro Ala Asp Gln His Leu Glu Phe			
	320	325	330	
35	tgc tgagcccaa agggcagggc caacattagg gagcccagca ggaggtgctg	1120		

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Cys

	tgctgagaag acttcctgga ggtgtttgtt gaacatatct gcagagcctt cccagactcc	1180
	tgcaaatcca acccatatca ggctgtaagt cagagcaggc aatgcagaag aggagaccag	1240
	accaaggggt cagctggggc taggacagtg agggctgcta gaggggctgg gcctctcttt	1300
5	gcacatggac actgggcccc tctctatatt gagtggctctg ttaacattca ttggtggctg	1360
	attccaaaag atgagagcca aagctgcacg gactcgagtc ctaggctgca cacctcacia	1420
	gcatctcttc tactgcattc tgttggtcga agcaagtcac aaccagcag attcaaggag	1480
	taaggaatag gateccccctc tggatgggag gagcagcaat gtcattattac aaaaggggtgt	1540
	ggacacatgc agggattctt actgccgtct ttgcaaacia tccacaaaaa cttaaaaaact	1600
10	aaaagcctga agcacaagca ctctccaccc caggcacaca caccctggaa ttcctgtgt	1660
	gacatggta ccaccaactgt gtgtcccgag gateccagct cagctttgca tcgtgccct	1720
	atctccctct cgtctctccc tgttgatccc tcatgcacag ccacagcgag ctgtctaaaa	1780
	cacaaagctg accgcgccat ttctactca gcatccttc atgacctcc attgtctcta	1840
	ggataggggt tggaccagtc tgaatccaga ggatcaggat ccagcaggaa ccagaggata	1900
15	atgtgaggag ggtttaaaaa ggaaccattt tttgaggtgt gtgcaactgt tccacctga	1960
	ggcctggaag gatgaatgga agcagcagtt cctgaaccag gaagactcat gtgtgggggc	2020
	cattgctggt caagggggcag gaacaggtct ggtgacctg caagggaggga gccaggagca	2080
	agcattccca ctccaccttc ctccattcag tctgtgcca agttccccac tgcctgagcc	2140
	caactagaag ctggagggaa ggagggcctg tggtgcagt ccaggcatgt aggcctcctg	2200
20	ggaaagggag aatggcaaag acaggcagag tggatctgga ggggtcaacg gaagacggaa	2260
	catgtccact tccaggcccg agcttctcag cctgccgttt gccactctcc agcatctggc	2320
	ccagcctgtc catctctatc tctcttctc ccttactccg tctctccatc actcggaacc	2380
	atgtgcatth ctttgtctca gctatattgt ctccactctg agttttttgcc catgatgttg	2440
	gatgccatgg aatgccatat cctccccatt atctccccct tgtctggata attctactc	2500
25	atctacaaat actgatttta tctgtgcaaa gaagtcttcc ccagtgcctc tggttgacag	2560
	gggtttcttc tggcttctcc agactttctg ttctccacc acagccctta gcacctggg	2620
	gaggaggtgt tgctgtccag gtaaatgtg cggcaatgcc cctgcctcta gtgactccc	2680
	tccagcctac ccacaaacag gacctgcac ctgtctcaca aataaaaactg aactcttgaa	2740
	atgggtg	2746
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	<212> DNA	
	<213> Homo sapiens	
35	<220>	

163/177

<221> CDS

<222> (32)...(835)

<400> 143

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	Met Ala Pro Trp Ala Leu Leu	
	1 5	
	agc cct ggg gtc ctg gtg cgg acc ggg cac acc gtg ctg acc tgg gga	100
	Ser Pro Gly Val Leu Val Arg Thr Gly His Thr Val Leu Thr Trp Gly	
10	10 15 20	
	atc acg ctg gtg ctc ttc ctg cac gat acc gag ctg cgg caa tgg gag	148
	Ile Thr Leu Val Leu Phe Leu His Asp Thr Glu Leu Arg Gln Trp Glu	
	25 30 35	
	gag cag ggg gag ctg ctc ctg ccc ctc acc ttc ctg ctc ctg gtg ctg	196
15	Glu Gln Gly Glu Leu Leu Leu Pro Leu Thr Phe Leu Leu Leu Val Leu	
	40 45 50 55	
	ggc tcc ctg ctg ctc tac ctc gct gtg tca ctc atg gac cct ggc tac	244
	Gly Ser Leu Leu Leu Tyr Leu Ala Val Ser Leu Met Asp Pro Gly Tyr	
	60 65 70	
20	gtg aat gtg cag ccc cag cct cag gag gag ctc aaa gag gag cag aca	292
	Val Asn Val Gln Pro Gln Pro Gln Glu Glu Leu Lys Glu Glu Gln Thr	
	75 80 85	
	gcc atg gtt cct cca gcc atc cct ctt cgg cgc tgc aga tac tgc ctg	340
	Ala Met Val Pro Pro Ala Ile Pro Leu Arg Arg Cys Arg Tyr Cys Leu	
25	90 95 100	
	gtg ctg cag ccc ctg agg gct cgg cac tgc cgt gag tgc cgc cgt tgc	388
	Val Leu Gln Pro Leu Arg Ala Arg His Cys Arg Glu Cys Arg Arg Cys	
	105 110 115	
	gtc cgc cgc tac gac cac cac tgc ccc tgg atg gag aac tgt gtg gga	436
30	Val Arg Arg Tyr Asp His His Cys Pro Trp Met Glu Asn Cys Val Gly	
	120 125 130 135	
	gag cgc aac cac cca ctc ttt gtg gtc tac ctg gcg ctg cag ctg gtg	484
	Glu Arg Asn His Pro Leu Phe Val Val Tyr Leu Ala Leu Gln Leu Val	
	140 145 150	
35	gtg ctt ctg tgg ggc ctg tac ctg gca tgg tca ggc ctc cgg ttc ttc	532

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Val Leu Leu Trp Gly Leu Tyr Leu Ala Trp Ser Gly Leu Arg Phe Phe
 155 160 165
 cag ccc tgg ggt ctg tgg ttg cgg tcc agc ggg ctc ctg ttc gcc acc 580
 Gln Pro Trp Gly Leu Trp Leu Arg Ser Ser Gly Leu Leu Phe Ala Thr
 5 170 175 180
 ttc ctg ctg ctg tcc ctc ttc tcg ttg gtg gcc agc ctg ctc ctc gtc 628
 Phe Leu Leu Leu Ser Leu Phe Ser Leu Val Ala Ser Leu Leu Leu Val
 185 190 195
 tcg cac ctc tac ctg gtg gcc agc aac acc acc acc tgg gaa ttc atc 676
 10 Ser His Leu Tyr Leu Val Ala Ser Asn Thr Thr Thr Trp Glu Phe Ile
 200 205 210 215
 tcc tca cac cgc atc gcc tat ctc cgc cag cgc ccc agc aac ccc ttc 724
 Ser Ser His Arg Ile Ala Tyr Leu Arg Gln Arg Pro Ser Asn Pro Phe
 220 225 230
 15 gac cga ggc ctg acc cgc aac ctg gcc cac ttc ttc tgt gga tgg ccc 772
 Asp Arg Gly Leu Thr Arg Asn Leu Ala His Phe Phe Cys Gly Trp Pro
 235 240 245
 tca ggg tcc tgg gag acc ctc tgg gct gag gag gag gaa gag ggc agc 820
 Ser Gly Ser Trp Glu Thr Leu Trp Ala Glu Glu Glu Glu Glu Gly Ser
 20 250 255 260
 agc cca gct gtt tagggttgct ggaggccggg ctaccgtctt gtgcctga 870
 Ser Pro Ala Val
 265
 aaaccacggg gcctgtcccc agctgggggtg agcgcctcaga gggcctgggg ccctcactcc 930
 25 tgcccacgcc tcccagaccc cagaacggag cttcaagtea gacagatccc tgccttggtg 990
 ggcagttctg ccttccaagg aagaagggga agaaaaggac ctgtgggtgg ctcaggccca 1050
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 atttaataata aagcaagtcc agtctt 1136
 30 <210> 144
 <211> 619
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 <213> Homo sapience
 <220>
 35 <221> CDS

$\langle 222 \rangle \quad (13) \dots (333)$

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Met Ser Thr Asn Asn Met Ser Asp Pro Arg Arg Pro

5

10

Asn Lys Val Leu Arg Tyr Lys Pro Pro Pro Ser Glu Cys Asn Pro Ala

20

25

Leu Asp Asp Pro Thr Pro Asp Tyr Met Asn Leu Leu Gly Met Ile Phe

35

40

Ser Met Cys Gly Leu Met Leu Lys Leu Lys Trp Cys Ala Trp Val Ala

45

50

55

60

Val Tyr Cys Ser Phe Ile Ser Phe Ala Asn Ser Arg Ser Ser Glu Asp

65

70

75

20

Thr Lys Gln Met Met Ser Ser Phe Met Leu Ser Ile Ser Ala Val Val

80

85

90

Met Ser Tyr Leu Gln Asn Pro Gln Pro Met Thr Pro Pro Trp

95

100

105

tgataccagc ctagaagggt cacattttgg accctgtcta tccactaggc ctgggcctttg 390

gctgctaaac ctgctgcctt cagctgccat cctggacttc cctgaatgag gccgtctcgg 450

tgccccagc tggatagagg gaacctggcc ctttcctagg gaacacccta ggcttaccce 510

tcctgcctcc ctteccctgc ctgctgctgg gggagatgct gtccatgttt ctaggggtat 570

tcatttgctt tctcgttgaa acctggtggt aataaagttt ttcaactcag 619

30

<210> 145

<211> 864

<212> DNA

<213> Homo sapience

35

<220>

166/177

<221> CDS

<222> (111)...(785)

<400> 145

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	gag	acg	ccg	cgc	ctc	gat	cc	cgc	gcg	ggc	ggg	acc	ggg	gc	cat	c	atg	acc			116
																		Met	Thr		
																			1		
	ctg	ttt	cac	ttc	ggg	aac	tgc	ttc	gct	ctt	gcc	tac	ttc	ccc	tac	ttc					164
10	Leu	Phe	His	Phe	Gly	Asn	Cys	Phe	Ala	Leu	Ala	Tyr	Phe	Pro	Tyr	Phe					
				5					10					15							
	atc	acc	tac	aag	tgc	agc	ggc	ctg	tcc	gag	tac	aac	gcc	ttc	tgg	aaa					212
	Ile	Thr	Tyr	Lys	Cys	Ser	Gly	Leu	Ser	Glu	Tyr	Asn	Ala	Phe	Trp	Lys					
				20				25					30								
15	tgc	gtc	cag	gct	gga	gtc	acc	tac	ctc	ttt	gtc	caa	ctc	tgc	aag	atg					260
	Cys	Val	Gln	Ala	Gly	Val	Thr	Tyr	Leu	Phe	Val	Gln	Leu	Cys	Lys	Met					
				35				40					45			50					
	ctg	ttc	ttg	gcc	act	ttc	ttt	ccc	acc	tgg	gaa	ggc	ggc	atc	tat	gac					308
	Leu	Phe	Leu	Ala	Thr	Phe	Phe	Pro	Thr	Trp	Glu	Gly	Gly	Ile	Tyr	Asp					
20					55				60					65							
	ttc	att	ggg	gag	ttc	atg	aag	gcc	agc	gtg	gat	gtg	gca	gac	ctg	ata					356
	Phe	Ile	Gly	Glu	Phe	Met	Lys	Ala	Ser	Val	Asp	Val	Ala	Asp	Leu	Ile					
					70				75					80							
	ggc	cta	aac	ctt	gtc	atg	tcc	cgg	aat	gcc	ggc	aag	gga	gag	tac	aag					404
25	Gly	Leu	Asn	Leu	Val	Met	Ser	Arg	Asn	Ala	Gly	Lys	Gly	Glu	Tyr	Lys					
				85				90					95								
	atc	atg	ggt	gct	gcc	ctg	ggc	tgg	gcc	act	gct	gag	ctt	att	atg	tcc					452
	Ile	Met	Val	Ala	Ala	Leu	Gly	Trp	Ala	Thr	Ala	Glu	Leu	Ile	Met	Ser					
				100				105					110								
30	cgc	tgc	att	ccc	cta	tgg	gtc	gga	gcc	cgg	ggc	att	gag	ttt	gac	tgg					500
	Arg	Cys	Ile	Pro	Leu	Trp	Val	Gly	Ala	Arg	Gly	Ile	Glu	Phe	Asp	Trp					
				115				120					125			130					
	aag	tac	atc	cag	atg	agc	ata	gac	tcc	aac	atc	agt	ctg	gtc	cat	tac					548
	Lys	Tyr	Ile	Gln	Met	Ser	Ile	Asp	Ser	Asn	Ile	Ser	Leu	Val	His	Tyr					
35					135				140					145							

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atc gtc gcg tct gct cag gtc tgg atg ata aca cgc tat gat ctg tac 596
 Ile Val Ala Ser Ala Gln Val Trp Met Ile Thr Arg Tyr Asp Leu Tyr
 150 155 160
 cac acc ttc cgg cca gct gtc ctc ctg ctg atg ttc ctc agt gtc tac 644
 5 His Thr Phe Arg Pro Ala Val Leu Leu Leu Met Phe Leu Ser Val Tyr
 165 170 175
 aag gcc ttt gtt atg gag acc ttc gtc cac ctc tgc tcg ctg ggc agt 692
 Lys Ala Phe Val Met Glu Thr Phe Val His Leu Cys Ser Leu Gly Ser
 180 185 190
 10 tgg gca gct cta ctg gcc cga gca gtg gta acg ggg ctg ctg gcc ctc 740
 Trp Ala Ala Leu Leu Ala Arg Ala Val Val Thr Gly Leu Leu Ala Leu
 195 200 205 210
 agc act ttg gcc ctg tat gtc gcc gtt gtc aat gtg cac tcc taggcttg 790
 Ser Thr Leu Ala Leu Tyr Val Ala Val Val Asn Val His Ser
 15 215 220
 gtgtctcaga cattgatgta ccttttcct gcctcgtcc aggttttagt gaagtaaaca 850
 gtatttgaa agtt 864

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 20 <211> 1527
 <212> DNA
 <213> Homo sapience
 <220>
 <221> CDS
 25 <222> (25)...(801)

 <400> 146
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 Met Ala Val Leu Ala Pro Leu Ile Ala
 30 1 5
 ctc gtg tat tcg gtg ccg cga ctt tca cga tgg ctc gcc caa cct tac 99
 Leu Val Tyr Ser Val Pro Arg Leu Ser Arg Trp Leu Ala Gln Pro Tyr
 10 15 20 25
 tac ctt ctg tcg gcc ctg ctc tct gct gcc ttc cta ctc gtg agg aaa 147
 35 Tyr Leu Leu Ser Ala Leu Leu Ser Ala Ala Phe Leu Leu Val Arg Lys

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	30	35	40	
	ctg ccg ccg ctc tgc cac ggt ctg ccc acc caa cgc gaa gac ggt aac			195
	Leu Pro Pro Leu Cys His Gly Leu Pro Thr Gln Arg Glu Asp Gly Asn			
	45	50	55	
5	ccg tgt gac ttt gac tgg aga gaa gtg gag atc ctg atg ttt ctc agt			243
	Pro Cys Asp Phe Asp Trp Arg Glu Val Glu Ile Leu Met Phe Leu Ser			
	60	65	70	
	gcc att gtg atg atg aag aac cgc aga tcc atg ttc ctg atg acg tgc			291
	Ala Ile Val Met Met Lys Asn Arg Arg Ser Met Phe Leu Met Thr Cys			
10	75	80	85	
	aaa ccc ccc cta tat atg ggc cct gag tat atc aag tac ttc aat gat			339
	Lys Pro Pro Leu Tyr Met Gly Pro Glu Tyr Ile Lys Tyr Phe Asn Asp			
	90	95	100	105
	aaa acc att gat gag gaa cta gaa cgg gac aag agg gtc act tgg att			387
15	Lys Thr Ile Asp Glu Glu Leu Glu Arg Asp Lys Arg Val Thr Trp Ile			
	110	115	120	
	gtg gag ttc ttt gcc aat tgg tct aat gac tgc caa tca ttt gcc cct			435
	Val Glu Phe Phe Ala Asn Trp Ser Asn Asp Cys Gln Ser Phe Ala Pro			
	125	130	135	
20	atc tat gct gac ctc tcc ctt aaa tac aac tgt aca ggg cta aat ttt			483
	Ile Tyr Ala Asp Leu Ser Leu Lys Tyr Asn Cys Thr Gly Leu Asn Phe			
	140	145	150	
	ggg aag gtg gat gtt gga cgc tat act gat gtt agt acg cgg tac aaa			531
	Gly Lys Val Asp Val Gly Arg Tyr Thr Asp Val Ser Thr Arg Tyr Lys			
25	155	160	165	
	gtg agc aca tca ccc ctc acc aag caa ctc cct acc ctg atc ctg ttc			579
	Val Ser Thr Ser Pro Leu Thr Lys Gln Leu Pro Thr Leu Ile Leu Phe			
	170	175	180	185
	caa ggt ggc aag gag gca atg cgg cgg cca cag att gac aag aaa gga			627
30	Gln Gly Gly Lys Glu Ala Met Arg Arg Pro Gln Ile Asp Lys Lys Gly			
	190	195	200	
	cgg gct gtc tca tgg acc ttc tct gag gag aat gtg atc cga gaa ttt			675
	Arg Ala Val Ser Trp Thr Phe Ser Glu Glu Asn Val Ile Arg Glu Phe			
	205	210	215	
35	aac tta aat gag cta tac cag cgg gcc aag aaa cta tca aag gct gga			723

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Asn Leu Asn Glu Leu Tyr Gln Arg Ala Lys Lys Leu Ser Lys Ala Gly
 220 225 230
 gac aat atc cct gag gag cag cct gtg gct tca acc ccc acc aca gtg 771
 Asp Asn Ile Pro Glu Glu Gln Pro Val Ala Ser Thr Pro Thr Thr Val
 5 235 240 245
 tca gat ggg gaa aac aag aag gat aaa taagatcctc ac 810
 Ser Asp Gly Glu Asn Lys Lys Asp Lys
 250 255
 tttggcagtg ctctctctcc tgtcaattcc aggetctttc cataaccaca agcctgagggc 870
 10 tgcagccttt tatttatgtt ttccctttgg ctgtgactgg gtggggcagc atgcagcttc 930
 tgattttaaa gaggcattcta gggaattgtc aggcacctta caggaaggcc tgccatgctg 990
 tggccaactg ttctactgga gcaagaaaga gatctcatag gacggagggg gaaatggttt 1050
 ccctccaagc ttgggtcagt gtgttaactg cttatcagct attcagacat ctccatggtt 1110
 tctccatgaa actctgtggt ttcattcattc cttcttagtt gacctgcaca gcttggttag 1170
 15 acctagattt aaccttaagg taagatgctg gggatatagaa cgctaagaat tttcccccaa 1230
 ggactcttgc ttcttaagc ccttctgget tegtattatgg tcttcattaa aagtataagc 1290
 ctaactttgt cgctagtcct aaggagaaac ctttaaccac aaagttttta tcattgaaga 1350
 caatattgaa caacccccta ttttgtgggg attgagaagg ggtgaataga ggcttgagac 1410
 tttcctttgt gtggtaggac ttggaggaga aatcccctgg actttcacta accctctgac 1470
 20 atactcccca caccagttg atggctttcc gtaataaaaa gattgggatt tcctttt 1527

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 <211> 659
 <212> DNA
 25 <213> Homo sapience
 <220>
 <221> CDS
 <222> (138)...(470)

 30 <400> 147
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 aagtagtggt tccggcgccg tgttccagct ccgcgttggt ccgcgagaaa gcgagagggc 120
 gagcccgggc tgggtgcg atg gcc gcg gtg gtg gcc aag cgg gaa ggg ccg 170
 Met Ala Ala Val Val Ala Lys Arg Glu Gly Pro
 35 1 5 10

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ccc ttc atc agc gag gcg gcc gtg cgg ggc aac gcc gcc gtc ctg gat 218
 Pro Phe Ile Ser Glu Ala Ala Val Arg Gly Asn Ala Ala Val Leu Asp
 15 20 25
 tat tgc cgg acc tcg gtg tca gcg ctg tcg ggg gcc acg gcc ggc atc 266
 5 Tyr Cys Arg Thr Ser Val Ser Ala Leu Ser Gly Ala Thr Ala Gly Ile
 30 35 40
 ctc ggc ctc acc ggc ctc tac ggc ttc atc ttc tac ctg ctc gcc tcc 314
 Leu Gly Leu Thr Gly Leu Tyr Gly Phe Ile Phe Tyr Leu Leu Ala Ser
 45 50 55
 10 gtc ctg ctc tcc ctg ctc ctc att ctc aag gcg gga agg agg tgg aac 362
 Val Leu Leu Ser Leu Leu Leu Ile Leu Lys Ala Gly Arg Arg Trp Asn
 60 65 70 75
 aaa tat ttc aaa tca cgg aga cct ctc ttt aca gga ggc ctc atc ggg 410
 Lys Tyr Phe Lys Ser Arg Arg Pro Leu Phe Thr Gly Gly Leu Ile Gly
 15 80 85 90
 ggc ctc ttc acc tac gtc ctg ttc tgg acg ttc ctc tac ggc atg gtg 458
 Gly Leu Phe Thr Tyr Val Leu Phe Trp Thr Phe Leu Tyr Gly Met Val
 95 100 105
 cac gtc tac tgaaatgggg gcccggggga cttttttaaa aaa 500
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(21) International Application Number: PCT/JP99/03929 (22) International Filing Date: 22 July 1999 (22.07.99) (30) Priority Data: <table><tr><td>10/208820</td><td>24 July 1998 (24.07.98)</td><td>JP</td></tr><tr><td>10/224105</td><td>7 August 1998 (07.08.98)</td><td>JP</td></tr><tr><td>10/238116</td><td>25 August 1998 (25.08.98)</td><td>JP</td></tr><tr><td>10/254736</td><td>9 September 1998 (09.09.98)</td><td>JP</td></tr><tr><td>10/275505</td><td>29 September 1998 (29.09.98)</td><td>JP</td></tr></table> (71) Applicants (for all designated States except US): SAGAMI CHEMICAL RESEARCH CENTER [JP/JP]; 4-1, Nishi-Onuma 4-chome, Sagamihara-shi, Kanagawa 229-0012 (JP). PROTEGENE INC. [JP/JP]; 2-20-3, Naka-cho, Meguro-ku, Tokyo 153-0065 (JP). (72) Inventors; and (75) Inventors/Applicants (for US only): KATO, Seishi [JP/JP]; 3-46-50, Wakamatsu, Sagamihara-shi, Kanagawa 229-0014 (JP). KIMURA, Tomoko [JP/JP]; 302, 4-1-28, Nishiikuta, Tama-ku, Kawasaki-shi, Kanagawa 214-0037 (JP).			10/208820	24 July 1998 (24.07.98)	JP	10/224105	7 August 1998 (07.08.98)	JP	10/238116	25 August 1998 (25.08.98)	JP	10/254736	9 September 1998 (09.09.98)	JP	10/275505	29 September 1998 (29.09.98)	JP	(74) Agents: AOYAMA, Tamotsu et al.; Aoyama & Partners, IMP Building, 3-7, Shiromi 1-chome, Chuo-ku, Osaka-shi. Osaka 540-0001 (JP). (81) Designated States: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZA, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SL, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG). Published <i>With international search report.</i> <i>Before the expiration of the time limit for amending the claims and to be republished in the event of the receipt of amendments.</i> (88) Date of publication of the international search report: 4 May 2000 (04.05.00)
10/208820	24 July 1998 (24.07.98)	JP																
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10/254736	9 September 1998 (09.09.98)	JP																
10/275505	29 September 1998 (29.09.98)	JP																
(54) Title: HUMAN PROTEINS HAVING HYDROPHOBIC DOMAINS AND DNAs ENCODING THESE PROTEINS																		
(57) Abstract <p>The present invention provides human proteins having hydrophobic domains, DNAs coding for these proteins, and expression vectors for these DNAs as well as eucaryotic cells expressing these DNAs.</p>																		

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EE	Estonia	LR	Liberia	SG	Singapore		

INTERNATIONAL SEARCH REPORT

International Application No

PC1, P 99/03929

A. CLASSIFICATION OF SUBJECT MATTER

IPC 7 C12N15/12 C07K14/705 C12N5/10

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 7 C12N C07K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 98 21328 A (KATO SEISHI ;PROTEGENE INC (JP); SEKINE SHINGO (JP); SAGAMI CHEM R) 22 May 1998 (1998-05-22) abstract page 17, last paragraph -page 18, paragraph 1 ---	1-6
X	DATABASE EMBLEMEST6 [Online] Accession Number AI057511, 22 July 1998 (1998-07-22) STRAUSBERG R: "H. sapiens cDNA clone IMAGE:1653181 3' similar to SW:YJK4 yeast P42929 hypothetical 16.2 kD protein in SME1-MEF2 intergenic region" XP002123564 100% identity in 357 BP overlap with SEQ ID NO:11 --- -/--	1-6



Further documents are listed in the continuation of box C.



Patent family members are listed in annex.

* Special categories of cited documents :

- *A* document defining the general state of the art which is not considered to be of particular relevance
- *E* earlier document but published on or after the international filing date
- *L* document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
- *O* document referring to an oral disclosure, use, exhibition or other means
- *P* document published prior to the international filing date but later than the priority date claimed

T later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

X document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

Y document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

& document member of the same patent family

Date of the actual completion of the international search

23 November 1999

Date of mailing of the international search report

06.03.00

Name and mailing address of the ISA

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Authorized officer

CUPIDO, M

INTERNATIONAL SEARCH REPORT

International Application No

PC JP 99/03929

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	<p>DATABASE EMBLEST21 [Online] Accession Number AA 482452, 24 June 1997 (1997-06-24) HILLIER L ET AL.: "zv05b11.r1 Soares NhHMPu S1 Homo sapiens cDNA clone 7527733 5'similar to SW:YJK4 yeast P42929 hypothetical 16.2 kD protein in SME1-MEF2 intergenic region" XP002123565 99.7% identity in 367 BP overlap with SEQ ID NO 11</p> <p>---</p>	1-6
A	<p>D'ANDREA ET AL: "Molecular Cloning of NKB1. A Natural Killer Cell Receptor for HLA -B Allotypes" JOURNAL OF IMMUNOLOGY, vol. 155, no. 5, 1 September 1995 (1995-09-01), pages 2306-2310 2310, XP002111500 ISSN: 0022-1767 abstract page 2307, right-hand column, line 16</p> <p>---</p>	1-6
A	<p>GILLEN C M ET AL: "Molecular cloning and functional expression of the K-Cl cotransporter from rabbit, rat, and human." JOURNAL OF BIOLOGICAL CHEMISTRY., vol. 271, no. 27, 5 July 1996 (1996-07-05), pages 16237-16244, XP002119528 AMERICAN SOCIETY OF BIOLOGICAL CHEMISTS, BALTIMORE, MD., US ISSN: 0021-9258 abstract</p> <p>---</p>	1-6
A	<p>KYTE J ET AL: "A SIMPLE METHOD FOR DISPLAYING THE HYDROPATHIC CHARACTER OF A PROTEIN" JOURNAL OF MOLECULAR BIOLOGY, vol. 157, no. 1, 5 May 1982 (1982-05-05), pages 105-132, XP000609692 ISSN: 0022-2836 cited in the application the whole document</p> <p>---</p>	1-6
P,X	<p>DATABASE EMBLEST11 [Online] Accession Number AI 553893, 25 March 1999 (1999-03-25) STRAUSBERG R: "Homo sapiens cDNA clone IMAGE:2169115 3'" XP002123566 100% identity in 375 BP overlap with SEQ ID 11</p> <p>-----</p>	1-6

INTERNATIONAL SEARCH REPORT

In ational application No

PCT/JP 99/ 03929

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☐ Claims Nos.:
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:

3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheets

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.

2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.

3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:

4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

1-6 partially

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest
- ☐ No protest accompanied the payment of additional search fees

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

1. Claims: Claims 1-6 partially

A protein comprising amino acid sequence SEQ ID NO 1, a DNA SEQ ID NO 11 or 21, encoding this protein, as well as an expression vector capable of expressing this sequence and a eukaryotic cell expressing the DNA

2. Claims: 1-6 partially

Idem as subject 1 but limited to protein SEQ ID NO. 2 and DNA SEQ ID 12 and 22

3. Claims: 1-6 partially

Idem as subject 1 but limited to protein SEQ ID NO. 3 and DNA SEQ ID 13 and 23

4. Claims: 1-6 partially

Idem as subject 1 but limited to protein SEQ ID NO. 4 and DNA SEQ ID 14 and 24

5. Claims: 1-6 partially

Idem as subject 1 but limited to protein SEQ ID NO. 5 and DNA SEQ ID 15 and 25

6. Claims: 1-6 partially

Idem as subject 1 but limited to protein SEQ ID NO. 6 and DNA SEQ ID 16 and 36

7. Claims: 1-6 partially

Idem as subject 1 but limited to protein SEQ ID NO. 7 and DNA SEQ ID 17 and 37

8. Claims: 1-6 partially

Idem as subject 1 but limited to protein SEQ ID NO. 8 and DNA SEQ ID 18 and 38

9. Claims: 1-6 partially

Idem as subject 1 but limited to protein SEQ ID NO. 9 and DNA SEQ ID 19 and 39

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

10. Claims: 1-6 partially

Idem as subject 1 but limited to protein SEQ ID NO. 10 and
DNA SEQ ID 20 and 30

11. Claims: 1-6 partially

Idem as subject 1 but limited to protein SEQ ID NO. 31 and
DNA SEQ ID 41 and 51

12. Claims: 1-6 partially

Idem as subject 1 but limited to protein SEQ ID NO. 32 and
DNA SEQ ID 42 and 52

13. Claims: 1-6 partially

Idem as subject 1 but limited to protein SEQ ID NO. 33 and
DNA SEQ ID 43 and 53

14. Claims: 1-6 partially

Idem as subject 1 but limited to protein SEQ ID NO. 34 and
DNA SEQ ID 44 and 54

15. Claims: 1-6 partially

Idem as subject 1 but limited to protein SEQ ID NO. 35 and
DNA SEQ ID 45 and 55

16. Claims: 1-6 partially

Idem as subject 1 but limited to protein SEQ ID NO. 36 and
DNA SEQ ID 46 and 56

17. Claims: 1-6 partially

Idem as subject 1 but limited to protein SEQ ID NO. 37 and
DNA SEQ ID 47 and 57

18. Claims: 1-6 partially

Idem as subject 1 but limited to protein SEQ ID NO. 38 and
DNA SEQ ID 48 and 58

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

19. Claims: 1-6 partially

Idem as subject 1 but limited to protein SEQ ID NO. 39 and
DNA SEQ ID 49 and 59

20. Claims: 1-6 partially

Idem as subject 1 but limited to protein SEQ ID NO. 40 and
DNA SEQ ID 50 and 60

21. Claims: 1-6 partially

Idem as subject 1 but limited to protein SEQ ID NO. 61 and
DNA SEQ ID 71 and 81

22. Claims: 1-6 partially

Idem as subject 1 but limited to protein SEQ ID NO. 62 and
DNA SEQ ID 72 and 82

23. Claims: 1-6 partially

Idem as subject 1 but limited to protein SEQ ID NO. 63 and
DNA SEQ ID 73 and 83

24. Claims: 1-6 partially

Idem as subject 1 but limited to protein SEQ ID NO. 64 and
DNA SEQ ID 74 and 84

25. Claims: 1-6 partially

Idem as subject 1 but limited to protein SEQ ID NO. 65 and
DNA SEQ ID 75 and 85

26. Claims: 1-6 partially

Idem as subject 1 but limited to protein SEQ ID NO. 66 and
DNA SEQ ID 76 and 86

27. Claims: 1-6 partially

Idem as subject 1 but limited to protein SEQ ID NO. 67 and
DNA SEQ ID 77 and 87

28. Claims: 1-6 partially

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

Idem as subject 1 but limited to protein SEQ ID NO. 68 and
DNA SEQ ID 78 and 88

29. Claims: 1-6 partially

Idem as subject 1 but limited to protein SEQ ID NO. 69 and
DNA SEQ ID 79 and 89

30. Claims: 1-6 partially

Idem as subject 1 but limited to protein SEQ ID NO. 70 and
DNA SEQ ID 80 and 90

31. Claims: 1-6 partially

Idem as subject 1 but limited to protein SEQ ID NO. 91 and
DNA SEQ ID 101 and 111

32. Claims: 1-6 partially

Idem as subject 1 but limited to protein SEQ ID NO. 92 and
DNA SEQ ID 102 and 112

33. Claims: 1-6 partially

Idem as subject 1 but limited to protein SEQ ID NO. 93 and
DNA SEQ ID 103 and 113

34. Claims: 1-6 partially

Idem as subject 1 but limited to protein SEQ ID NO. 94 and
DNA SEQ ID 104 and 114

35. Claims: 1-6 partially

Idem as subject 1 but limited to protein SEQ ID NO. 95 and
DNA SEQ ID 105 and 115

36. Claims: 1-6 partially

Idem as subject 1 but limited to protein SEQ ID NO. 96 and
DNA SEQ ID 106 and 116

37. Claims: 1-6 partially

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

Idem as subject 1 but limited to protein SEQ ID NO. 97 and
DNA SEQ ID 107 and 117

38. Claims: 1-6 partially

Idem as subject 1 but limited to protein SEQ ID NO. 98 and
DNA SEQ ID 108 and 118

39. Claims: 1-6 partially

Idem as subject 1 but limited to protein SEQ ID NO. 99 and
DNA SEQ ID 109 and 119

40. Claims: 1-6 partially

Idem as subject 1 but limited to protein SEQ ID NO. 100 and
DNA SEQ ID 110 and 120

41. Claims: 1-6 partially

Idem as subject 1 but limited to protein SEQ ID NO. 121 and
DNA SEQ ID 131 and 141

42. Claims: 1-6 partially

Idem as subject 1 but limited to protein SEQ ID NO. 122 and
DNA SEQ ID 132 and 142

43. Claims: 1-6 partially

Idem as subject 1 but limited to protein SEQ ID NO. 123 and
DNA SEQ ID 133 and 143

44. Claims: 1-6 partially

Idem as subject 1 but limited to protein SEQ ID NO. 124 and
DNA SEQ ID 134 and 144

45. Claims: 1-6 partially

Idem as subject 1 but limited to protein SEQ ID NO. 125 and
DNA SEQ ID 135 and 145

46. Claims: 1-6 partially

Idem as subject 1 but limited to protein SEQ ID NO. 126 and

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

DNA SEQ ID 136 and 146

47. Claims: 1-6 partially

Idem as subject 1 but limited to protein SEQ ID NO. 127 and
DNA SEQ ID 137 and 147

48. Claims: 1-6 partially

Idem as subject 1 but limited to protein SEQ ID NO. 128 and
DNA SEQ ID 138 and 148

49. Claims: 1-6 partially

Idem as subject 1 but limited to protein SEQ ID NO. 129 and
DNA SEQ ID 139 and 149

50. Claims: 1-6 partially

Idem as subject 1 but limited to protein SEQ ID NO. 130 and
DNA SEQ ID 140 and 150



INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No

PC JP 99/03929

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
WO 9821328 A	22-05-1998	AU 4885297 A EP 0941320 A	03-06-1998 15-09-1999
